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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 18:29:48 ; Search time 1867.5 Seconds
(without alignments)
450.960 Million cell updates/sec

Title: US-10-018-716B-2
Perfect score: 18
Sequence: 1 auaauuauggcccugcuc 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	94.4	794	1	AJ641058	AJ641058 AJ641058
c 2	16	88.9	312	2	BE153987	BE153987 PM0-HT033
c 3	16	88.9	340	3	BI432519	BI432519 EST535280
c 4	16	88.9	439	8	T14826	T14826 crs268 lamb
5	16	88.9	500	3	BP191026	BP191026 BP191026
c 6	16	88.9	652	2	BG600462	BG600462 EST505357
c 7	16	88.9	740	8	CX409188	CX409188 JGI_XZT32
8	16	88.9	747	10	CL169941	CL169941 104_370_1
c 9	16	88.9	752	10	CW385975	CW385975 fsbb001f0
c 10	16	88.9	759	2	BG889203	BG889203 EST515054
c 11	16	88.9	761	10	CL169940	CL169940 104_370_1
12	16	88.9	1030	10	CL033121	CL033121 CH216-36A
13	15	83.3	85	6	CD963839	CD963839 SDY_133 G
c 14	15	83.3	95	10	CG560188	CG560188 OST180267
c 15	15	83.3	102	10	CG671007	CG671007 OST472166
16	15	83.3	208	7	CO323095	CO323095 EK189652.
c 17	15	83.3	238	10	CG556891	CG556891 OST172871
c 18	15	83.3	247	8	CX626914	CX626914 GAN008N05
c 19	15	83.3	285	3	BI491822	BI491822 df15e12.w
20	15	83.3	306	2	BF353376	BF353376 QV1-HT063
21	15	83.3	308	2	BG184004	BG184004 RST2919 A
22	15	83.3	336	2	BG790049	BG790049 sae62d11.
23	15	83.3	345	3	BM443576	BM443576 EBro02_SQ
24	15	83.3	346	2	BB710886	BB710886 BB710886
c 25	15	83.3	348	5	BU019684	BU019684 QHE22N11.
26	15	83.3	365	7	CO190893	CO190893 EK050016.
27	15	83.3	374	1	AW020862	AW020862 df15e12.y
c 28	15	83.3	401	10	AB082236	AB082236 Drosophil
c 29	15	83.3	405	9	BH388002	BH388002 AG-ND-151
30	15	83.3	435	2	BG181938	BG181938 RST797 At
31	15	83.3	437	1	AW317773	AW317773 sg57b02.y
32	15	83.3	441	2	BG187151	BG187151 RST6134 A
c 33	15	83.3	444	5	BQ977181	BQ977181 QHI24C10.
34	15	83.3	445	6	CA938690	CA938690 sav36e03.
35	15	83.3	446	5	BU761255	BU761255 sas65d07.
36	15	83.3	449	9	AQ631994	AQ631994 RPCI-11-4
37	15	83.3	452	2	BG205213	BG205213 RST24640
c 38	15	83.3	465	2	BI071352	BI071352 C056P39U
c 39	15	83.3	471	2	BG187152	BG187152 RST6135 A
40	15	83.3	476	1	AW099240	AW099240 sd37a01.y
c 41	15	83.3	496	8	DN650903	DN650903 G7045.80
42	15	83.3	501	2	BG214697	BG214697 RST34346
c 43	15	83.3	511	1	AI150588	AI150588 qf36g07.x
c 44	15	83.3	516	1	AL900125	AL900125 AL900125
c 45	15	83.3	533	8	DN650904	DN650904 G7072.54

ALIGNMENTS

RESULT 1
AJ641058
LOCUS AJ641058 794 bp mRNA linear EST 28-JAN-2005
DEFINITION AJ641058 Populus tremula x P. tremuloides/Amanita muscaria mixed EST library Populus tremula x P. tremuloides/Amanita muscaria mixed EST library cDNA clone ptamabc210068e03, mRNA sequence.
ACCESSION AJ641058
VERSION AJ641058.1 GI:58309785
KEYWORDS EST.
SOURCE Populus tremula x P. tremuloides/Amanita muscaria mixed EST library
ORGANISM Populus tremula x P. tremuloides/Amanita muscaria mixed EST library
Eukaryota; mixed EST libraries.
REFERENCE 1 (bases 1 to 794)
AUTHORS Bekel,T., Meyer,F., Kuester,H., Manthey,K., Perlick,A., Puehler,A., Bock,A. and Nehls,U.
TITLE ESTs of fully developed ectomycorrhizas formed between Populus tremula x tremuloides and Amanita muscaria
JOURNAL Unpublished (2005)
COMMENT Contact: Bekel T.
Physiologische Oekologie der Pflanzen
Eberhard-Karls-Universitaet
Auf der Morgenstelle 1, Tuebingen, BW 72076, Germany.
FEATURES Location/Qualifiers
source 1. .794
/organism="Populus tremula x P. tremuloides/Amanita muscaria mixed EST library"
/mol_type="mRNA"
/db_xref="taxon:143775"
/clone="ptamabc210068e03"
/clone_lib="Populus tremula x P. tremuloides/Amanita muscaria mixed EST library"
ORIGIN

Query Match 94.4%; Score 17; DB 1; Length 794;
Best Local Similarity 64.7%; Pred. No. 28;
Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AUAAUUAUGGCCCUGCU 17
              |:||::|:|||||:||:
Db        453 ATAATTATGGCCCTGCT 469
```

RESULT 2
BE153987/c
LOCUS BE153987 312 bp mRNA linear EST 21-JUN-2000

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DEFINITION  PM0-HT0339-060400-009-C04 HT0339 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE153987
VERSION     BE153987.1  GI:8616617
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 312)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM0-HT0339-060
            400-009-C04&t3=2000-04-06&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 7
            High quality sequence stop: 226.
FEATURES             Location/Qualifiers
     source          1. .312
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0339"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 2;  Length 312;
  Best Local Similarity   68.8%;  Pred. No. 1e+02;
  Matches   11;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGC 16
              |:||::|:|||||:||
Db        289 ATAATTATGGCCCTGC 274


RESULT 3
BI432519/c
LOCUS       BI432519                340 bp    mRNA    linear   EST 30-APR-2003
DEFINITION  EST535280 P. infestans-challenged potato leaf, compatible reaction
            Solanum tuberosum cDNA clone PPCAR82 5' sequence, mRNA sequence.
ACCESSION   BI432519
VERSION     BI432519.1  GI:15257209
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,
            Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B.
  TITLE     Generation of ESTs from Potato Leaves Challenged with Phytophthora
            infestans, Compatible Interaction
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/
            Seq primer: M13F-R.
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="PPCAR82"
                     /tissue_type="leaf"
                     /dev_stage="6 week old"
                     /lab_host="SOLR"
                     /clone_lib="P. infestans-challenged potato leaf,
                     compatible reaction"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; supplier: Cornell University, Fry lab; sequencing:
                     The Institute for Genomic Research; Whole plants were
                     challenged with 20,000 sporangia/ml of the compatible P.
                     infestans isolate US 940480.  Leaf tissue was collected at
                     3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen
                     in liquid nitrogen immediately upon removal.  Kennebec
                     plants showed first symptoms of infection at 48 hours
                     after inoculation.  NOTE: We cannot exclude the
                     possibility that this sequence is actually derived from
                     Phytophthora rather than potato."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 3;  Length 340;
  Best Local Similarity   68.8%;  Pred. No. 1e+02;
  Matches   11;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAUUAUGGCCCUGCUC 18
              ||::|:|||||:||:|
Db        283 AATTATGGCCCTGCTC 268


RESULT 4
T14826/c
LOCUS       T14826                  439 bp    mRNA    linear   EST 28-JUL-1995
DEFINITION  crs268 lambdaZAPST Ricinus communis cDNA clone pcrs268, mRNA
            sequence.
ACCESSION   T14826
VERSION     T14826.1  GI:688463
KEYWORDS    EST.
SOURCE      Ricinus communis (castor bean)
  ORGANISM  Ricinus communis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae;
            Acalypheae; Ricinus.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   vandeLoo,F.J., Turner,S. and Somerville,C.
  TITLE     Expressed sequence tags from developing castor seeds
  JOURNAL   Plant Physiol. 108, 1141-1150 (1995)
COMMENT     Contact: Somerville CR
            Carnegie Institution
            Carnegie Institution, 290 Panama St, Stanford, CA 94305
            Tel: 4153251521
            Email: crs@andrew.stanford.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
```

```
     source          1. .439
                     /organism="Ricinus communis"
                     /mol_type="mRNA"
                     /strain="Baker 296"
                     /db_xref="taxon:3988"
                     /clone="pcrs268"
                     /clone_lib="lambdaZAPST"
                     /note="Vector: lambdaZAPII; Site_1: EcoR1; Site_2: XhoI;
                     Poly(A)+ RNA was purified from developing stage III to
                     stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
                     1982) endosperm plus embryo of immature castor fruits.
                     cDNA was synthesized and cloned into lambdaZAPII according
                     to the instructions of the manufacturer (Stratagene):
                     synthesis was primed from the poly(A) tail, and cloned
                     directionally into XhoI (3') and EcoRI (5') sites.  In few
                     cases, sequence data indicated that this directionality
                     was reversed.  Partial cDNA clones predominate. "
ORIGIN

  Query Match             88.9%;  Score 16;  DB 8;  Length 439;
  Best Local Similarity   68.8%;  Pred. No. 1e+02;
  Matches   11;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAUUAUGGCCCUGCUC 18
              ||::|:|||||:||:|
Db        332 AATTATGGCCCTGCTC 317


RESULT 5
BP191026
LOCUS       BP191026                 500 bp    mRNA    linear   EST 17-JUL-2003
DEFINITION  BP191026 planarian head cDNA Dugesia japonica cDNA clone 06171_HH,
            mRNA sequence.
ACCESSION   BP191026
VERSION     BP191026.1  GI:32905550
KEYWORDS    EST.
SOURCE      Dugesia japonica
  ORGANISM  Dugesia japonica
            Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata;
            Tricladida; Paludicola; Dugesiidae; Dugesia.
REFERENCE   1  (bases 1 to 500)
  AUTHORS   Mineta,K., Nakazawa,M., Cebria,F., Ikeo,K., Agata,K. and
            Gojobori,T.
  TITLE     Origin and evolutionary process of the CNS elucidated by
            comparative genomics analysis of planarian ESTs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7666-7671 (2003)
   PUBMED   12802012
COMMENT     Contact: Katsuhiko Mineta
            National Institute of Genetics, Center for Information Biology and
            DNA Data Bank of Japan
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6847
            Fax: 81-559-81-6848
            Email: kmineta@lab.nig.ac.jp
            These clones and additional information are obtained from our web
            site: http://www.cib.nig.ac.jp/dda/.
FEATURES             Location/Qualifiers
     source          1. .500
                     /organism="Dugesia japonica"
                     /mol_type="mRNA"
                     /db_xref="taxon:6161"
                     /clone="06171_HH"
                     /tissue_type="head"
                     /dev_stage="adult"
                     /clone_lib="planarian head cDNA"
ORIGIN

  Query Match             88.9%;  Score 16;  DB 3;  Length 500;
  Best Local Similarity   62.5%;  Pred. No. 1e+02;
  Matches   10;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UAAUUAUGGCCCUGCU 17
              :||::|:|||||:||:
Db        353 TAATTATGGCCCTGCT 368


RESULT 6
BG600462/c
LOCUS       BG600462                 652 bp    mRNA    linear   EST 07-MAR-2003
DEFINITION  EST505357 cSTS Solanum tuberosum cDNA clone cSTS29I1 5' sequence,
            mRNA sequence.
ACCESSION   BG600462
VERSION     BG600462.1  GI:13617598
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 652)
  AUTHORS   van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
            Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
  TITLE     Generations of ESTs from sprouting potato eyes
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/
            Seq primer: M13F-R.
FEATURES             Location/Qualifiers
     source          1. .652
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="cSTS29I1"
                     /tissue_type="sprouting eyes from tubers"
                     /dev_stage="12-14 weeks post harvest"
                     /lab_host="SOLR"
                     /clone_lib="cSTS"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
                     taken from tubers. The tubers were incubated at 26C in the
                     dark for 2-3 weeks prior to sprouting. The eyes were
                     frozen in liquid nitrogen immediately upon removal from
                     tubers."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 2;  Length 652;
  Best Local Similarity   68.8%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAUUAUGGCCCUGCUC 18
              ||::|:|||||:||:|
Db        536 AATTATGGCCCTGCTC 521


RESULT 7
CX409188/c
LOCUS       CX409188                 740 bp    mRNA    linear   EST 06-JAN-2005
DEFINITION  JGI_XZT32096.fwd NIH_XGC_tropTad5 Xenopus tropicalis cDNA clone
            IMAGE:7608418 5', mRNA sequence.
ACCESSION   CX409188
VERSION     CX409188.1  GI:57189890
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 740)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
```

```
  TITLE     DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Richard M. Harland Laboratory, University of
            California, Berkeley: http://tropicalis.berkeley.edu/home
            cDNA Library Preparation: Richard M. Harland Laboratory, University
            of California, Berkeley
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Clone Distribution: I.M.A.G.E. Consortium/LLNL:
            http://image.llnl.gov
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
            indicates a forward sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Plate: XZT 0333  row: o  column: 8
            High quality sequence stop: 706.
FEATURES             Location/Qualifiers
     source          1. .740
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:7608418"
                     /tissue_type="whole embryo"
                     /dev_stage="Tadpole (st. 36-41)"
                     /lab_host="E. coli XL1-Blue derivative, Stratagene
                     ElectroTen-Blue"
                     /clone_lib="NIH_XGC_tropTad5"
                     /note="Vector: pCS108; Site_1: SalI; Site_2: NotI; Tadpole
                     library constructed by Russell B. Fletcher in R. Harland's
                     lab using poly A RNA and oligo dT primers (Invitrogen
                     SuperScript Plasmid System for cDNA Synthesis and
                     Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
                     into vector pCS108
                     (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
                     ."
ORIGIN

  Query Match            88.9%;  Score 16;  DB 8;  Length 740;
  Best Local Similarity   68.8%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGC 16
              |:||::|:|||||:||
Db         43 ATAATTATGGCCCTGC 28


RESULT 8
CL169941
LOCUS       CL169941                747 bp    DNA     linear   GSS 06-JAN-2004
DEFINITION  104_370_10813405_148_31788_109 Sorghum methylation-filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10813405, genomic survey
            sequence.
ACCESSION   CL169941
VERSION     CL169941.1  GI:40682353
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 370  row: e  column: 13
            Seq primer: SWfor Forward
            Class: methylation filtered
            High quality sequence stop: 747.
FEATURES             Location/Qualifiers
     source          1. .747
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10813405"
                     /clone_lib="Sorghum methylation-filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation-filtered library."
ORIGIN

  Query Match            88.9%;  Score 16;  DB 10;  Length 747;
  Best Local Similarity   62.5%;  Pred. No. 1.1e+02;
  Matches   10;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UAAUUAUGGCCCUGCU 17
              :||::|:|||||:||:
Db        387 TAATTATGGCCCTGCT 402


RESULT 9
CW385975/c
LOCUS       CW385975                752 bp    DNA     linear   GSS 01-NOV-2004
DEFINITION  fsbb001f069k13k0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fsbb001f069k13, genomic survey
            sequence.
ACCESSION   CW385975
VERSION     CW385975.1  GI:55104419
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 752)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: fsbb001f069  row: k  column: 13
            Seq primer: k Reverse
            Class: methylation filtered
            High quality sequence stop: 752.
FEATURES             Location/Qualifiers
     source          1. .752
                     /organism="Sorghum bicolor"
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                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="fsbb001f069k13"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 10;  Length 752;
  Best Local Similarity   62.5%;  Pred. No. 1.1e+02;
  Matches   10;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UAAUUAUGGCCCUGCU 17
              :||::|:|||||:||:
Db        614 TAATTATGGCCCTGCT 599


RESULT 10
BG889203/c
LOCUS       BG889203                759 bp    mRNA    linear   EST 07-MAR-2003
DEFINITION  EST515054 cSTD Solanum tuberosum cDNA clone cSTD13G2 5' sequence,
            mRNA sequence.
ACCESSION   BG889203
VERSION     BG889203.1  GI:14266289
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemingo,A.,
            Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
  TITLE     Generations of ESTs from dormant potato tubers
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/
            Seq primer: M13F-R.
FEATURES             Location/Qualifiers
     source          1. .759
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="cSTD13G2"
                     /tissue_type="dormant tuber"
                     /dev_stage="one month post-harvest"
                     /lab_host="SOLR"
                     /clone_lib="cSTD"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; This library targets genes expressed in dormant
                     tubers. This library was made from sections of dormant
                     tuber, avoiding the buds and epidermis. Tubers were stored
                     for one month post-harvest at 4oC. The tuber was peeled,
                     well away from the surface. Then it was chopped into 1-2
                     mm cubes and immediately frozen in liquid nitrogen. This
                     library is noted as P4 in Tanksley lab notebooks."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 2;  Length 759;
  Best Local Similarity   68.8%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAUUAUGGCCCUGCUC 18
              ||::|:|||||:||:|
Db        621 AATTATGGCCCTGCTC 606


RESULT 11
CL169940/c
LOCUS       CL169940                761 bp    DNA     linear   GSS 06-JAN-2004
DEFINITION  104_370_10813405_116_31789_109 Sorghum methylation-filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10813405, genomic survey
            sequence.
ACCESSION   CL169940
VERSION     CL169940.1  GI:40682352
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 761)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 370  row: e  column: 13
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 761.
FEATURES             Location/Qualifiers
     source          1. .761
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10813405"
                     /clone_lib="Sorghum methylation-filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation-filtered library."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 10;  Length 761;
  Best Local Similarity   62.5%;  Pred. No. 1.1e+02;
  Matches   10;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UAAUUAUGGCCCUGCU 17
              :||::|:|||||:||:
Db        654 TAATTATGGCCCTGCT 639


RESULT 12
CL033121
LOCUS       CL033121                1030 bp    DNA     linear   GSS 31-DEC-2003
DEFINITION  CH216-36A12_Sp6.1 CH216 Xenopus tropicalis genomic clone
            CH216-36A12, genomic survey sequence.
ACCESSION   CL033121
VERSION     CL033121.1  GI:40483484
KEYWORDS    GSS.
```

```
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 1030)
  AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
  TITLE     A physical map of the xenopus tropicalis genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 175000   Std Error: 0.00
            Seq primer: Sp6 ATTTAGGTGACACTATAG
            Class: BAC ends
            High quality sequence start: 29
            High quality sequence stop: 943.
FEATURES             Location/Qualifiers
     source          1. .1030
                     /organism="Xenopus tropicalis"
                     /mol_type="genomic DNA"
                     /strain="Nigerian frog"
                     /db_xref="taxon:8364"
                     /clone="CH216-36A12"
                     /sex="male"
                     /cell_line="Stock 248 F7A2, inbred N7"
                     /clone_lib="CH216"
                     /note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                     BAC library"
ORIGIN

  Query Match             88.9%;  Score 16;  DB 10;  Length 1030;
  Best Local Similarity   68.8%;  Pred. No. 1.1e+02;
  Matches   11;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGC 16
              |:||::|:|||||:||
Db         32 ATAATTATGGCCCTGC 47


RESULT 13
CD963839
LOCUS       CD963839                 85 bp    mRNA    linear   EST 16-JUL-2003
DEFINITION  SDY_133 GeneTag2 Zea mays cDNA, mRNA sequence.
ACCESSION   CD963839
VERSION     CD963839.1  GI:32824117
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 85)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .85
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="mixture"
                     /db_xref="taxon:4577"
                     /clone_lib="GeneTag2"
ORIGIN

  Query Match             83.3%;  Score 15;  DB 6;  Length 85;
  Best Local Similarity   66.7%;  Pred. No. 3.8e+02;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 AUUAUGGCCCUGCUC 18
              |::|:|||||:||:|
Db         47 ATTATGGCCCTGCTC 61


RESULT 14
CG560188/c
LOCUS       CG560188                 95 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST180267 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST180267,
            mRNA sequence.
ACCESSION   CG560188
VERSION     CG560188.1  GI:37346775
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 95)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
   PUBMED   14610273
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .95
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST180267"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             83.3%;  Score 15;  DB 10;  Length 95;
  Best Local Similarity   66.7%;  Pred. No. 3.8e+02;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UAAUUAUGGCCCUGC 16
              :||::|:|||||:||
Db         51 TAATTATGGCCCTGC 37


RESULT 15
CG671007/c
LOCUS       CG671007                102 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST472166 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST472166,
            mRNA sequence.
ACCESSION   CG671007
VERSION     CG671007.1  GI:37494856
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
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```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 102)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
   PUBMED   14610273
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .102
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST472166"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             83.3%;  Score 15;  DB 10;  Length 102;
  Best Local Similarity   66.7%;  Pred. No. 3.8e+02;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UAAUUAUGGCCCUGC 16
              :||::|:|||||:||
Db         42 TAATTATGGCCCTGC 28


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Job time : 1867.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 17:06:31 ; Search time 136.5 Seconds
(without alignments)
19.597 Million cell updates/sec

Title: US-10-018-716B-2
Perfect score: 18
Sequence: 1 auaauuauggcccugcuc 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3205263 seqs, 74304013 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_New:*
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9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	14	77.8	1149	9	US-11-082-389-213	Sequence 213, App
	2	12	66.7	19	8	US-11-101-244-173294	Sequence 173294,
c	3	12	66.7	19	8	US-11-101-244-339765	Sequence 339765,
	4	12	66.7	19	8	US-11-101-244-600029	Sequence 600029,
	5	12	66.7	19	8	US-11-101-244-1044082	Sequence 1044082,
	6	12	66.7	19	8	US-11-101-244-1044118	Sequence 1044118,
	7	12	66.7	19	8	US-11-101-244-1152178	Sequence 1152178,
	8	12	66.7	19	8	US-11-101-244-1152276	Sequence 1152276,
	9	12	66.7	19	8	US-11-101-244-1311535	Sequence 1311535,
c	10	12	66.7	19	8	US-11-101-244-1430673	Sequence 1430673,
c	11	12	66.7	19	8	US-11-101-244-1430674	Sequence 1430674,
	12	12	66.7	19	9	US-11-083-784-173294	Sequence 173294,
c	13	12	66.7	19	9	US-11-083-784-339765	Sequence 339765,
	14	12	66.7	19	9	US-11-083-784-600029	Sequence 600029,
	15	12	66.7	19	9	US-11-083-784-1044082	Sequence 1044082,
	16	12	66.7	19	9	US-11-083-784-1044118	Sequence 1044118,
	17	12	66.7	19	9	US-11-083-784-1152178	Sequence 1152178,
	18	12	66.7	19	9	US-11-083-784-1152276	Sequence 1152276,
	19	12	66.7	19	9	US-11-083-784-1311535	Sequence 1311535,
c	20	12	66.7	19	9	US-11-083-784-1430673	Sequence 1430673,
c	21	12	66.7	19	9	US-11-083-784-1430674	Sequence 1430674,
c	22	12	66.7	844	9	US-11-082-389-441	Sequence 441, App
c	23	12	66.7	1095	9	US-11-082-389-439	Sequence 439, App
	24	12	66.7	1656	1	US-10-131-826A-239	Sequence 239, App
c	25	12	66.7	3458	1	US-10-793-626-3510	Sequence 3510, Ap
	26	12	66.7	6708	1	US-10-821-234-164	Sequence 164, App
	27	12	66.7	7382	1	US-10-839-211-1	Sequence 1, Appli
	28	11	61.1	19	8	US-11-101-244-341877	Sequence 341877,
c	29	11	61.1	19	8	US-11-101-244-343613	Sequence 343613,
c	30	11	61.1	19	8	US-11-101-244-343631	Sequence 343631,
c	31	11	61.1	19	8	US-11-101-244-374101	Sequence 374101,
c	32	11	61.1	19	8	US-11-101-244-380293	Sequence 380293,
c	33	11	61.1	19	8	US-11-101-244-425500	Sequence 425500,
c	34	11	61.1	19	8	US-11-101-244-425510	Sequence 425510,
c	35	11	61.1	19	8	US-11-101-244-425572	Sequence 425572,
c	36	11	61.1	19	8	US-11-101-244-661639	Sequence 661639,
c	37	11	61.1	19	8	US-11-101-244-661697	Sequence 661697,
	38	11	61.1	19	8	US-11-101-244-716963	Sequence 716963,
	39	11	61.1	19	8	US-11-101-244-716974	Sequence 716974,
c	40	11	61.1	19	8	US-11-101-244-725866	Sequence 725866,
c	41	11	61.1	19	8	US-11-101-244-764763	Sequence 764763,
c	42	11	61.1	19	8	US-11-101-244-764784	Sequence 764784,
c	43	11	61.1	19	8	US-11-101-244-764830	Sequence 764830,
c	44	11	61.1	19	8	US-11-101-244-799257	Sequence 799257,
c	45	11	61.1	19	8	US-11-101-244-828288	Sequence 828288,

ALIGNMENTS

RESULT 1
US-11-082-389-213
; Sequence 213, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 213
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1126)
; OTHER INFORMATION: RXN00523

US-11-082-389-213

Query Match 77.8%; Score 14; DB 9; Length 1149;
Best Local Similarity 64.3%; Pred. No. 2.3;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 UUAUGGCCCUGCUC 18
              ::|:|||||:||:|
Db        229 TTATGGCCCTGCTC 242
```

RESULT 2
US-11-101-244-173294
; Sequence 173294, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 173294
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-173294

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 UAUGGCCCUGCU 17
              ||||||||||||
Db          3 UAUGGCCCUGCU 14
```

RESULT 3
US-11-101-244-339765/c
; Sequence 339765, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 339765
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-339765

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 8; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 UAAUUAUGGCCC 13
              :||::|:|||||
Db         19 TAATTATGGCCC 8
```

RESULT 4
US-11-101-244-600029
; Sequence 600029, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 600029
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-600029

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 AUGGCCCUGCUC 18
              ||||||||||||
Db          3 AUGGCCCUGCUC 14
```

RESULT 5
US-11-101-244-1044082
; Sequence 1044082, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1044082
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1044082

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 AUGGCCCUGCUC 18
              ||||||||||||
Db          3 AUGGCCCUGCUC 14
```

RESULT 6
US-11-101-244-1044118
; Sequence 1044118, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1044118
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1044118

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 AUGGCCCUGCUC 18
              ||||||||||||
Db          5 AUGGCCCUGCUC 16
```

RESULT 7
US-11-101-244-1152178
; Sequence 1152178, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1152178
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1152178

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 AUGGCCCUGCUC 18
              ||||||||||||
Db          5 AUGGCCCUGCUC 16
```

RESULT 8
US-11-101-244-1152276
; Sequence 1152276, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1152276
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1152276

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 AUGGCCCUGCUC 18
              ||||||||||||
Db          5 AUGGCCCUGCUC 16
```

RESULT 9
US-11-101-244-1311535
; Sequence 1311535, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1311535
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1311535

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;

```
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCC 12
              ||||||||||||
Db          3 AUAAUUAUGGCC 14


RESULT 10
US-11-101-244-1430673/c
; Sequence 1430673, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1430673
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1430673

  Query Match             66.7%;  Score 12;  DB 8;  Length 19;
  Best Local Similarity   75.0%;  Pred. No. 34;
  Matches    9;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AUGGCCCUGCUC 18
              |:|||||:||:|
Db         12 ATGGCCCTGCTC 1


RESULT 11
US-11-101-244-1430674/c
; Sequence 1430674, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1430674
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1430674

  Query Match             66.7%;  Score 12;  DB 8;  Length 19;
  Best Local Similarity   75.0%;  Pred. No. 34;
  Matches    9;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AUGGCCCUGCUC 18
              |:|||||:||:|
Db         15 ATGGCCCTGCTC 4


RESULT 12
US-11-083-784-173294
; Sequence 173294, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 173294
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-173294

  Query Match             66.7%;  Score 12;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 UAUGGCCCUGCU 17
              ||||||||||||
Db          3 UAUGGCCCUGCU 14


RESULT 13
US-11-083-784-339765/c
; Sequence 339765, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 339765
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-339765
```

```
  Query Match             66.7%;  Score 12;  DB 9;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 34;
  Matches    8;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UAAUUAUGGCCC 13
              :||::|:|||||
Db         19 TAATTATGGCCC 8


RESULT 14
US-11-083-784-600029
; Sequence 600029, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 600029
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-600029

  Query Match             66.7%;  Score 12;  DB 9;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 34;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AUGGCCCUGCUC 18
              ||||||||||||
Db          3 AUGGCCCUGCUC 14


RESULT 15
US-11-083-784-1044082
; Sequence 1044082, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1044082
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1044082

  Query Match             66.7%;  Score 12;  DB 9;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 34;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 AUGGCCCUGCUC 18
              ||||||||||||
Db          3 AUGGCCCUGCUC 14


Search completed: November 29, 2005, 18:29:39
Job time : 136.5 secs
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 17:06:31 ; Search time 72 Seconds
(without alignments)
444.390 Million cell updates/sec

Title: US-10-018-716B-2
Perfect score: 18
Sequence: 1 auaauuauggcccugcuc 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	2179	2	US-08-487-886-1	Sequence 1, Appli
	2	18	100.0	2179	2	US-08-531-070A-1	Sequence 1, Appli
	3	18	100.0	2179	3	US-08-482-855-1	Sequence 1, Appli
	4	18	100.0	2179	3	US-08-474-986-1	Sequence 1, Appli
	5	18	100.0	2393	3	US-09-016-434-1209	Sequence 1209, Ap
	6	15	83.3	481	3	US-09-270-767-1666	Sequence 1666, Ap
	7	15	83.3	481	3	US-09-270-767-16948	Sequence 16948, A
c	8	15	83.3	52992	3	US-09-949-016-16105	Sequence 16105, A
	9	14	77.8	900	3	US-09-489-039A-6996	Sequence 6996, Ap
	10	14	77.8	1149	3	US-09-602-787A-379	Sequence 379, App
c	11	14	77.8	1887	3	US-09-620-312D-42	Sequence 42, Appl
	12	14	77.8	3678	3	US-09-112-580-13	Sequence 13, Appl
c	13	14	77.8	3762	3	US-09-489-039A-4926	Sequence 4926, Ap
	14	14	77.8	55264	3	US-09-949-016-15014	Sequence 15014, A
c	15	14	77.8	70828	3	US-09-949-016-12122	Sequence 12122, A
	16	14	77.8	94755	3	US-09-949-016-11839	Sequence 11839, A
	17	14	77.8	101951	3	US-09-949-016-15648	Sequence 15648, A
	18	14	77.8	137226	3	US-09-949-016-13763	Sequence 13763, A
c	19	14	77.8	139936	3	US-09-949-016-11782	Sequence 11782, A
c	20	14	77.8	139952	3	US-09-949-016-13280	Sequence 13280, A
	21	14	77.8	147840	3	US-09-949-016-15236	Sequence 15236, A
	22	13	72.2	25	3	US-09-396-196G-44948	Sequence 44948, A
	23	13	72.2	339	3	US-09-489-039A-6054	Sequence 6054, Ap
c	24	13	72.2	459	3	US-09-248-796A-1604	Sequence 1604, Ap
	25	13	72.2	601	3	US-09-949-016-48726	Sequence 48726, A
c	26	13	72.2	601	3	US-09-949-016-156620	Sequence 156620,
	27	13	72.2	601	3	US-09-949-016-160355	Sequence 160355,
	28	13	72.2	601	3	US-09-949-016-160356	Sequence 160356,
	29	13	72.2	668	3	US-09-533-559-5223	Sequence 5223, Ap
	30	13	72.2	886	2	US-08-469-427A-1	Sequence 1, Appli
	31	13	72.2	886	2	US-08-609-443B-1	Sequence 1, Appli
	32	13	72.2	886	2	US-08-569-063C-1	Sequence 1, Appli
	33	13	72.2	886	3	US-08-851-896-1	Sequence 1, Appli
	34	13	72.2	1443	3	US-09-489-039A-5874	Sequence 5874, Ap
	35	13	72.2	2554	3	US-09-701-868-4	Sequence 4, Appli
c	36	13	72.2	7883	3	US-09-949-016-13183	Sequence 13183, A
	37	13	72.2	8773	3	US-09-949-016-14496	Sequence 14496, A
c	38	13	72.2	9792	3	US-09-635-872A-14	Sequence 14, Appl
c	39	13	72.2	9792	3	US-09-636-077A-14	Sequence 14, Appl
c	40	13	72.2	9792	3	US-09-636-060C-14	Sequence 14, Appl
c	41	13	72.2	9792	3	US-09-986-552-14	Sequence 14, Appl
c	42	13	72.2	9792	3	US-09-636-596C-14	Sequence 14, Appl
c	43	13	72.2	9792	3	US-10-023-894-21	Sequence 21, Appl
c	44	13	72.2	9792	3	US-10-306-686-14	Sequence 14, Appl
c	45	13	72.2	9792	3	US-09-895-072-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-487-886-1
; Sequence 1, Application US/08487886
; Patent No. 5744448
; GENERAL INFORMATION:
; APPLICANT: Kelton, Christie Ann
; APPLICANT: Schweickhardt, Rene Lynn
; APPLICANT: Cheng, Shirley Vui Yen
; APPLICANT: Nugent, No. 5744448een Patrice
; TITLE OF INVENTION: Human Follicle Stimulating
; TITLE OF INVENTION: Hormone Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephan P. Williams,
; ADDRESSEE: Ares-Serono, Inc.
; STREET: Exchange Place, 37th floor
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
; COMPUTER: IBM PS/2, model 55 SX
; OPERATING SYSTEM: MS-DOS version 4.0
; SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/670,085
; FILING DATE: 15-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Stephan P.
; REGISTRATION NUMBER: 28546
; REFERENCE/DOCKET NUMBER: US/252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-1300
; TELEFAX: (617) 723-8923
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2179
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:

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;       ORGANISM:  Homo sapiens
;       TISSUE TYPE:  Testis
;     IMMEDIATE SOURCE:
;       LIBRARY:  lgt11 cDNA library, ClonTech #HL1010b
;       CLONE:  pHFSHR11-11, pHFSHR15-6
;     FEATURE:
;       NAME/KEY:  protein coding region
;       LOCATION:  75 to 2159
US-08-487-886-1

  Query Match             100.0%;  Score 18;  DB 2;  Length 2179;
  Best Local Similarity   66.7%;  Pred. No. 0.21;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         69 ATAATTATGGCCCTGCTC 86


RESULT 2
US-08-531-070A-1
; Sequence 1, Application US/08531070A
; Patent No. 5851768
;  GENERAL INFORMATION:
;    APPLICANT:  de la Chapelle, Albert
;    APPLICANT:  Aittomaki, Kristiina
;    APPLICANT:  Huhtaniemi, Ilpo
;    TITLE OF INVENTION:  Method For Diagnosis Of Ovarian Dysgenesis
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/531,070A
;      FILING DATE:  20-SEP-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gass, David A.
;      REGISTRATION NUMBER:  38,153
;      REFERENCE/DOCKET NUMBER:  28113/32879
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2179 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-531-070A-1

  Query Match             100.0%;  Score 18;  DB 2;  Length 2179;
  Best Local Similarity   66.7%;  Pred. No. 0.21;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         69 ATAATTATGGCCCTGCTC 86


RESULT 3
US-08-482-855-1
; Sequence 1, Application US/08482855
; Patent No. 6121016
;  GENERAL INFORMATION:
;    APPLICANT:  Kelton, Christie Ann
;    APPLICANT:  Schweickhardt, Rene Lynn
;    APPLICANT:  Cheng, Shirley Vui Yen
;    APPLICANT:  Nugent, No. 6121016een Patrice
;    TITLE OF INVENTION:  Human Follicle Stimulating
;    TITLE OF INVENTION:  Hormone Receptor
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephan P. Williams,
;      ADDRESSEE:  Ares-Serono, Inc.
;      STREET:  Exchange Place, 37th floor
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" diskette, 1.44 MB, high density
;      COMPUTER:  IBM PS/2, model 55 SX
;      OPERATING SYSTEM:  MS-DOS version 4.0
;      SOFTWARE:  VAX/VMS Mass11 via Kermit to IBM MS-DOS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,855
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/670,085
;      FILING DATE:  15-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Stephan P.
;      REGISTRATION NUMBER:  28546
;      REFERENCE/DOCKET NUMBER:  US/252
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 723-1300
;      TELEFAX:  (617) 723-8923
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2179
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  Testis
;    IMMEDIATE SOURCE:
;      LIBRARY:  lgt11 cDNA library, ClonTech #HL1010b
;      CLONE:  pHFSHR11-11, pHFSHR15-6
;    FEATURE:
;      NAME/KEY:  protein coding region
;      LOCATION:  75 to 2159
US-08-482-855-1

  Query Match             100.0%;  Score 18;  DB 3;  Length 2179;
  Best Local Similarity   66.7%;  Pred. No. 0.21;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         69 ATAATTATGGCCCTGCTC 86


RESULT 4
US-08-474-986-1
; Sequence 1, Application US/08474986
; Patent No. 6372711
;  GENERAL INFORMATION:
;       APPLICANT: Kelton, Christie Ann
;                  Schweickhardt, Rene Lynn
;                  Cheng, Shirley Vui Yen
;                  Nugent, No. 6372711een Patrice
```

```
;       TITLE OF INVENTION: Human Follicle Stimulating
;                           Hormone Receptor
;       NUMBER OF SEQUENCES: 2
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Stephan P. Williams,
;                       Ares-Serono, Inc.
;            STREET: Exchange Place, 37th floor
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
;            COMPUTER: IBM PS/2, model 55 SX
;            OPERATING SYSTEM: MS-DOS version 4.0
;            SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/474,986
;            FILING DATE: 07-Jun-1995
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 07/670,085
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Williams, Stephan P.
;            REGISTRATION NUMBER: 28546
;            REFERENCE/DOCKET NUMBER: US/252
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617) 723-1300
;            TELEFAX: (617) 723-8923
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2179
;            TYPE: Nucleic acid
;            STRANDEDNESS: Double
;            TOPOLOGY: Linear
;       MOLECULE TYPE: cDNA to mRNA
;       ORIGINAL SOURCE:
;            ORGANISM: Homo sapiens
;            TISSUE TYPE: Testis
;       IMMEDIATE SOURCE:
;            LIBRARY: lgt11 cDNA library, ClonTech #HL1010b
;            CLONE: pHFSHR11-11, pHFSHR15-6
;       FEATURE:
;            NAME/KEY:  protein coding region
;            LOCATION:  75 to 2159
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-474-986-1

  Query Match             100.0%;  Score 18;  DB 3;  Length 2179;
  Best Local Similarity   66.7%;  Pred. No. 0.21;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         69 ATAATTATGGCCCTGCTC 86


RESULT 5
US-09-016-434-1209
; Sequence 1209, Application US/09016434
; Patent No. 6500938
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1209:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2393 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g182770
US-09-016-434-1209

  Query Match             100.0%;  Score 18;  DB 3;  Length 2393;
  Best Local Similarity   66.7%;  Pred. No. 0.21;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78


RESULT 6
US-09-270-767-1666
; Sequence 1666, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1666
;   LENGTH: 481
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-1666

  Query Match             83.3%;  Score 15;  DB 3;  Length 481;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 AUUAUGGCCCUGCUC 18
              |::|:|||||:||:|
Db        185 ATTATGGCCCTGCTC 199


RESULT 7
US-09-270-767-16948
; Sequence 16948, Application US/09270767
; Patent No. 6703491
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; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16948
;    LENGTH: 481
;    TYPE: DNA
;    ORGANISM: Drosophila melanogaster
US-09-270-767-16948

  Query Match             83.3%;  Score 15;  DB 3;  Length 481;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 AUUAUGGCCCUGCUC 18
              |::|:|||||:||:|
Db        185 ATTATGGCCCTGCTC 199


RESULT 8
US-09-949-016-16105/c
; Sequence 16105, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16105
;    LENGTH: 52992
;    TYPE: DNA
;    ORGANISM: Human
US-09-949-016-16105

  Query Match             83.3%;  Score 15;  DB 3;  Length 52992;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUG 15
              |:||::|:|||||:|
Db       1241 ATAATTATGGCCCTG 1227


RESULT 9
US-09-489-039A-6996
; Sequence 6996, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 6996
;    LENGTH: 900
;    TYPE: DNA
;    ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6996

  Query Match             77.8%;  Score 14;  DB 3;  Length 900;
  Best Local Similarity   64.3%;  Pred. No. 45;
  Matches    9;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 AUUAUGGCCCUGCU 17
              |::|:|||||:||:
Db        124 ATTATGGCCCTGCT 137


RESULT 10
US-09-602-787A-379
; Sequence 379, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kr"ger, Burkhard
;  APPLICANT:  Sch"der, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CP
;  CURRENT APPLICATION NUMBER: US/09/602,787A
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932182.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932190.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932191.4
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932209.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932212.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932227.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932228.7
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932229.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932230.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932927.3
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933005.0
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933006.9
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19940764.9
;  PRIOR FILING DATE: 1999-08-27
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;  PRIOR APPLICATION NUMBER: DE 19940765.7
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940766.5
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940830.0
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940831.9
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940832.7
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19940833.5
;  PRIOR FILING DATE: 1999-08-27
;  PRIOR APPLICATION NUMBER: DE 19941378.9
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19941379.7
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19941395.9
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19942077.7
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942078.5
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942079.3
;  PRIOR FILING DATE: 1999-09-03
;  PRIOR APPLICATION NUMBER: DE 19942088.2
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 379
;   LENGTH: 1149
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(1126)
;   OTHER INFORMATION: RXN00523
US-09-602-787A-379

  Query Match             77.8%;  Score 14;  DB 3;  Length 1149;
  Best Local Similarity   64.3%;  Pred. No. 45;
  Matches    9;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 UUAUGGCCCUGCUC 18
              ::|:|||||:||:|
Db        229 TTATGGCCCTGCTC 242


RESULT 11
US-09-620-312D-42/c
; Sequence 42, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  John Tillinghast
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: No. 6569662el Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 784CIP2B
;  CURRENT APPLICATION NUMBER: US/09/620,312D
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER: 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 1105
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 42
;   LENGTH: 1887
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (55)..(1563)
US-09-620-312D-42

  Query Match             77.8%;  Score 14;  DB 3;  Length 1887;
  Best Local Similarity   64.3%;  Pred. No. 45;
  Matches    9;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 AUUAUGGCCCUGCU 17
              |::|:|||||:||:
Db        896 ATTATGGCCCTGCT 883


RESULT 12
US-09-112-580-13
; Sequence 13, Application US/09112580
; Patent No. 6610539
; GENERAL INFORMATION:
;  APPLICANT: WRIGHT, Jim A.
;  APPLICANT: YOUNG, Aiping
;  APPLICANT: DUGOURD, Dominique
;  TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF
;  TITLE OF INVENTION: MICROORGANISMS
;  FILE REFERENCE: 032396-016
;  CURRENT APPLICATION NUMBER: US/09/112,580
;  CURRENT FILING DATE: 1998-07-09
;  EARLIER APPLICATION NUMBER: US 60/052,160
;  EARLIER FILING DATE: 1997-07-10
;  NUMBER OF SEQ ID NOS: 265
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 3678
;   TYPE: DNA
;   ORGANISM: Equine herpesvirus 4
US-09-112-580-13

  Query Match             77.8%;  Score 14;  DB 3;  Length 3678;
  Best Local Similarity   64.3%;  Pred. No. 45;
  Matches    9;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCU 14
              |:||::|:|||||:
Db       2479 ATAATTATGGCCCT 2492


RESULT 13
US-09-489-039A-4926/c
; Sequence 4926, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 4926
;   LENGTH: 3762
;   TYPE: DNA
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```
;   ORGANISM: Klebsiella pneumoniae
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1044),(1659)
;   OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-489-039A-4926

  Query Match             77.8%;  Score 14;  DB 3;  Length 3762;
  Best Local Similarity   64.3%;  Pred. No. 45;
  Matches    9;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 UUAUGGCCCUGCUC 18
              ::|:|||||:||:|
Db       3722 TTATGGCCCTGCTC 3709


RESULT 14
US-09-949-016-15014
; Sequence 15014, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15014
;   LENGTH: 55264
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15014

  Query Match             77.8%;  Score 14;  DB 3;  Length 55264;
  Best Local Similarity   64.3%;  Pred. No. 45;
  Matches    9;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UAAUUAUGGCCCUG 15
              :||::|:|||||:|
Db      41065 TAATTATGGCCCTG 41078


RESULT 15
US-09-949-016-12122/c
; Sequence 12122, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12122
;   LENGTH: 70828
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(70828)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12122

  Query Match             77.8%;  Score 14;  DB 3;  Length 70828;
  Best Local Similarity   64.3%;  Pred. No. 45;
  Matches    9;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UAAUUAUGGCCCUG 15
              :||::|:|||||:|
Db      35413 TAATTATGGCCCTG 35400


Search completed: November 29, 2005, 18:25:00
Job time : 73 secs
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 17:06:35 ; Search time 403.5 Seconds
(without alignments)
368.894 Million cell updates/sec

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Perfect score: 18
Sequence: 1 auaauuauggcccugcuc 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	441	4	US-09-925-065A-192589	Sequence 192589,
	2	18	100.0	441	4	US-09-925-065A-192590	Sequence 192590,
	3	18	100.0	1922	8	US-10-349-528-4	Sequence 4, Appli
	4	18	100.0	2019	7	US-10-382-248-9	Sequence 9, Appli
	5	18	100.0	2393	5	US-10-225-567A-121	Sequence 121, App
	6	18	100.0	2393	5	US-10-207-655-64	Sequence 64, Appl
	7	18	100.0	2393	6	US-10-305-720-1209	Sequence 1209, Ap
	8	16	88.9	201	8	US-10-719-993-38475	Sequence 38475, A
	9	16	88.9	612	4	US-09-925-065A-391076	Sequence 391076,
	10	16	88.9	261638	8	US-10-719-993-6882	Sequence 6882, Ap
	11	15	83.3	461	4	US-09-925-065A-328046	Sequence 328046,
c	12	15	83.3	507	6	US-10-172-118-2085	Sequence 2085, Ap
c	13	15	83.3	507	7	US-10-342-887-2085	Sequence 2085, Ap
c	14	15	83.3	533	4	US-09-925-065A-520324	Sequence 520324,
c	15	15	83.3	544	4	US-09-925-065A-539398	Sequence 539398,
	16	15	83.3	612	5	US-10-007-280A-106	Sequence 106, App
	17	15	83.3	628	5	US-10-007-280A-107	Sequence 107, App
c	18	15	83.3	842	5	US-10-027-632-160723	Sequence 160723,
c	19	15	83.3	842	5	US-10-027-632-160724	Sequence 160724,
c	20	15	83.3	842	6	US-10-027-632-160723	Sequence 160723,
c	21	15	83.3	842	6	US-10-027-632-160724	Sequence 160724,
	22	15	83.3	1634	7	US-10-424-599-84619	Sequence 84619, A
c	23	15	83.3	2021	8	US-10-739-930-4619	Sequence 4619, Ap
	24	15	83.3	3659	10	US-11-097-143-15251	Sequence 15251, A
	25	15	83.3	9140	10	US-11-097-143-15250	Sequence 15250, A
c	26	15	83.3	76829	9	US-10-737-082-27	Sequence 27, Appl
c	27	15	83.3	76829	9	US-10-765-790-27	Sequence 27, Appl
	28	15	83.3	180227	7	US-10-322-281-308	Sequence 308, App
	29	15	83.3	202251	5	US-10-087-192-985	Sequence 985, App
c	30	15	83.3	325348	6	US-10-085-117-358	Sequence 358, App
	31	14	77.8	25	8	US-10-719-900-825663	Sequence 825663,
c	32	14	77.8	219	7	US-10-437-963-7570	Sequence 7570, Ap
	33	14	77.8	285	8	US-10-425-115-95091	Sequence 95091, A
	34	14	77.8	465	4	US-09-925-065A-622260	Sequence 622260,
	35	14	77.8	465	4	US-09-925-065A-622261	Sequence 622261,
	36	14	77.8	465	4	US-09-925-065A-622262	Sequence 622262,
c	37	14	77.8	574	5	US-10-066-543-3296	Sequence 3296, Ap
	38	14	77.8	591	5	US-10-027-632-15415	Sequence 15415, A
	39	14	77.8	591	5	US-10-027-632-15416	Sequence 15416, A
	40	14	77.8	591	6	US-10-027-632-15415	Sequence 15415, A
	41	14	77.8	591	6	US-10-027-632-15416	Sequence 15416, A
c	42	14	77.8	600	4	US-09-925-065A-895996	Sequence 895996,
c	43	14	77.8	611	5	US-10-027-632-224562	Sequence 224562,
c	44	14	77.8	611	6	US-10-027-632-224562	Sequence 224562,
	45	14	77.8	668	7	US-10-437-963-3301	Sequence 3301, Ap

ALIGNMENTS

RESULT 1
US-09-925-065A-192589
; Sequence 192589, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 192589
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-192589

Query Match 100.0%; Score 18; DB 4; Length 441;
Best Local Similarity 66.7%; Pred. No. 0.47;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db        318 ATAATTATGGCCCTGCTC 335
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RESULT 2
US-09-925-065A-192590
; Sequence 192590, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

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;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 192590
;   LENGTH: 441
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-192590

  Query Match            100.0%;  Score 18;  DB 4;  Length 441;
  Best Local Similarity   66.7%;  Pred. No. 0.47;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db        318 ATAATTATGGCCCTGCTC 335


RESULT 3
US-10-349-528-4
; Sequence 4, Application US/10349528
; Publication No. US20040253668A1
; GENERAL INFORMATION:
;  APPLICANT: RAMANATHAN, Chandra
;  APPLICANT:  GOPAL, Shuba
;  APPLICANT:  MINTIER, Gabe
;  APPLICANT:  FEDER, John
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
;  TITLE OF INVENTION:  USE THEREOF
;  FILE REFERENCE: D0210
;  CURRENT APPLICATION NUMBER: US/10/349,528
;  CURRENT FILING DATE:  2003-01-22
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 1922
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-10-349-528-4

  Query Match            100.0%;  Score 18;  DB 8;  Length 1922;
  Best Local Similarity   66.7%;  Pred. No. 0.48;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         11 ATAATTATGGCCCTGCTC 28


RESULT 4
US-10-382-248-9
; Sequence 9, Application US/10382248
; Publication No. US20040058347A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-568C
;  CURRENT APPLICATION NUMBER: US/10/382,248
;  CURRENT FILING DATE:  2003-03-05
;  PRIOR APPLICATION NUMBER: 60/366,928
;  PRIOR FILING DATE: 2002-03-22
;  PRIOR APPLICATION NUMBER: 60/361,974
;  PRIOR FILING DATE: 2002-03-06
;  PRIOR APPLICATION NUMBER: 60/365,477
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 60/401,661
;  PRIOR FILING DATE: 2002-08-06
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 9
;   LENGTH: 2019
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (61)..(1959)
US-10-382-248-9

  Query Match            100.0%;  Score 18;  DB 7;  Length 2019;
  Best Local Similarity   66.7%;  Pred. No. 0.48;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         55 ATAATTATGGCCCTGCTC 72


RESULT 5
US-10-225-567A-121
; Sequence 121, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
;   LENGTH: 2393
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-225-567A-121

  Query Match            100.0%;  Score 18;  DB 5;  Length 2393;
  Best Local Similarity   66.7%;  Pred. No. 0.48;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78


RESULT 6
US-10-207-655-64
; Sequence 64, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 64
;   LENGTH: 2393
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-207-655-64

  Query Match             100.0%;  Score 18;  DB 5;  Length 2393;
  Best Local Similarity   66.7%;  Pred. No. 0.48;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78


RESULT 7
US-10-305-720-1209
; Sequence 1209, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
;  APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
;  TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic
;  FILE REFERENCE: PA-0002-1 CON
;  CURRENT APPLICATION NUMBER: US/10/305,720
;  CURRENT FILING DATE:  2002-11-26
;  PRIOR APPLICATION NUMBER: 09/016,434
;  PRIOR FILING DATE: 1998-01-30
;  NUMBER OF SEQ ID NOS: 1490
;  SOFTWARE: PERL Program
; SEQ ID NO 1209
;   LENGTH: 2393
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GenBank ID No. US20040010136A1 g182770
US-10-305-720-1209

  Query Match             100.0%;  Score 18;  DB 6;  Length 2393;
  Best Local Similarity   66.7%;  Pred. No. 0.48;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78


RESULT 8
US-10-719-993-38475
; Sequence 38475, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001496
;  CURRENT APPLICATION NUMBER: US/10/719,993
;  CURRENT FILING DATE:  2003-11-24
;  NUMBER OF SEQ ID NOS: 55342
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38475
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-719-993-38475

  Query Match             88.9%;  Score 16;  DB 8;  Length 201;
  Best Local Similarity   68.8%;  Pred. No. 7.7;
  Matches   11;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGC 16
              |:||::|:|||||:||
Db        113 ATAATTATGGCCCTGC 128


RESULT 9
US-09-925-065A-391076
; Sequence 391076, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 391076
;   LENGTH: 612
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-391076

  Query Match             88.9%;  Score 16;  DB 4;  Length 612;
  Best Local Similarity   62.5%;  Pred. No. 7.8;
  Matches   10;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 UAAUUAUGGCCCUGCU 17
              :||::|:|||||:||:
Db        565 TAATTATGGCCCTGCT 580


RESULT 10
US-10-719-993-6882
; Sequence 6882, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001496
;  CURRENT APPLICATION NUMBER: US/10/719,993
;  CURRENT FILING DATE:  2003-11-24
;  NUMBER OF SEQ ID NOS: 55342
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6882
;   LENGTH: 261638
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-719-993-6882

  Query Match             88.9%;  Score 16;  DB 8;  Length 261638;
  Best Local Similarity   68.8%;  Pred. No. 8.4;
  Matches   11;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGC 16
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Db      29139 ATAATTATGGCCCTGC 29154


RESULT 11
US-09-925-065A-328046
; Sequence 328046, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
```

```
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 328046
;   LENGTH: 461
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-328046

  Query Match             83.3%;  Score 15;  DB 4;  Length 461;
  Best Local Similarity   66.7%;  Pred. No. 32;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAUUAUGGCCCUGCU 17
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Db         11 AATTATGGCCCTGCT 25


RESULT 12
US-10-172-118-2085/c
; Sequence 2085, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
;  APPLICANT: Dai, Hongyue
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Chris
;  APPLICANT:  Van 't Veer, Laura
;  APPLICANT:  Van de Vijver, Marc
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-175-999
;  CURRENT APPLICATION NUMBER: US/10/172,118
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/380,770
;  PRIOR FILING DATE: 2002-05-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2085
;   LENGTH: 507
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: Contig23454
;   DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-2085

  Query Match             83.3%;  Score 15;  DB 6;  Length 507;
  Best Local Similarity   66.7%;  Pred. No. 32;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAUUAUGGCCCUGCU 17
              ||::|:|||||:||:
Db        177 AATTATGGCCCTGCT 163


RESULT 13
US-10-342-887-2085/c
; Sequence 2085, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
;  APPLICANT: Dai, Hongyue
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter S.
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Christopher J.
;  APPLICANT:  Van 't Veer, Laura Johanna
;  APPLICANT:  Van de Vijver, Marc J.
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-188-999
;  CURRENT APPLICATION NUMBER: US/10/342,887
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: 60/298,918
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: 60/380,710
;  PRIOR FILING DATE: 2002-05-14
;  PRIOR APPLICATION NUMBER: 10/172,118
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2085
;   LENGTH: 507
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-342-887-2085

  Query Match             83.3%;  Score 15;  DB 7;  Length 507;
  Best Local Similarity   66.7%;  Pred. No. 32;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAUUAUGGCCCUGCU 17
              ||::|:|||||:||:
Db        177 AATTATGGCCCTGCT 163


RESULT 14
US-09-925-065A-520324/c
; Sequence 520324, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 520324
;   LENGTH: 533
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-520324

  Query Match             83.3%;  Score 15;  DB 4;  Length 533;
  Best Local Similarity   66.7%;  Pred. No. 32;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAUUAUGGCCCUGCU 17
              ||::|:|||||:||:
Db        368 AATTATGGCCCTGCT 354
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RESULT 15
US-09-925-065A-539398/c
; Sequence 539398, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 539398
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-539398

Query Match 83.3%; Score 15; DB 4; Length 544;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Qy          3 AAUUAUGGCCCUGCU 17
              ||::|:|||||:||:
Db        368 AATTATGGCCCTGCT 354
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Job time : 404.5 secs

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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 18:25:08 ; Search time 894.5 Seconds
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Perfect score: 18
Sequence: 1 auaauuauggcccugcuc 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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14: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	856	8	HSFSTHR	X68044 H.sapiens m
	2	18	100.0	1724	8	S73199	S73199 follicle-st
	3	18	100.0	1734	8	HSFSHX1	Z34260 H.sapiens D
	4	18	100.0	2179	6	AR003719	AR003719 Sequence
	5	18	100.0	2179	6	AR067576	AR067576 Sequence
	6	18	100.0	2179	6	AR207283	AR207283 Sequence
	7	18	100.0	2179	8	S59900	S59900 follicle st
	8	18	100.0	2186	8	HUMFSHREC	M95489 H.sapiens f
	9	18	100.0	2222	6	A76125	A76125 Sequence 1
	10	18	100.0	2374	6	CQ715054	CQ715054 Sequence
	11	18	100.0	2393	6	AR270646	AR270646 Sequence
	12	18	100.0	2393	6	AX548836	AX548836 Sequence
	13	18	100.0	2393	8	HUMFSHRE	M65085 Human folli
c	14	18	100.0	121688	8	AC092533	AC092533 Homo sapi
c	15	18	100.0	158709	14	AC083827	AC083827 Homo sapi
	16	17	94.4	162	8	HSFSHRX1	X91738 H.sapiens g
	17	16	88.9	1041	5	AY625217	AY625217 Priotelus
c	18	16	88.9	95681	8	AL157890	AL157890 Human DNA
	19	16	88.9	113657	14	AC166226	AC166226 Sorex ara
	20	16	88.9	121589	14	AC137655	AC137655 Bos tauru
	21	16	88.9	125311	8	AC068758	AC068758 Homo sapi
	22	16	88.9	127015	14	AC151504	AC151504 Dasypus n
	23	16	88.9	160179	14	AC092930	AC092930 Homo sapi
	24	16	88.9	168380	8	AC063933	AC063933 Homo sapi
	25	16	88.9	169314	14	AC148413	AC148413 Callithri
	26	16	88.9	169996	14	AC053521	AC053521 Homo sapi
c	27	16	88.9	171267	14	AC154087	AC154087 Alligator
	28	16	88.9	171990	14	AC153783	AC153783 Rhinoloph
	29	16	88.9	185798	14	AC158248	AC158248 Callithri
	30	16	88.9	187465	9	AC132305	AC132305 Mus muscu
	31	16	88.9	191709	9	AC115890	AC115890 Mus muscu
c	32	16	88.9	197909	9	AC158658	AC158658 Mus muscu
	33	16	88.9	198551	9	AC068605	AC068605 Mus muscu
	34	16	88.9	210236	14	AC150699	AC150699 Bos tauru
	35	16	88.9	236157	14	AC111356	AC111356 Rattus no
	36	16	88.9	256499	14	AC130987	AC130987 Rattus no
	37	16	88.9	283919	14	AC095169	AC095169 Rattus no
	38	15	83.3	481	6	AR496706	AR496706 Sequence
	39	15	83.3	481	6	AR511988	AR511988 Sequence
	40	15	83.3	612	6	AX554759	AX554759 Sequence
	41	15	83.3	628	6	AX554760	AX554760 Sequence
	42	15	83.3	1303	5	CR760514	CR760514 Xenopus t
	43	15	83.3	1437	5	BC061373	BC061373 Xenopus t
c	44	15	83.3	1727	15	AB023467	AB023467 Metschnik
c	45	15	83.3	2652	8	BC034230	BC034230 Homo sapi

ALIGNMENTS

RESULT 1
HSFSTHR
LOCUS HSFSTHR 856 bp mRNA linear PRI 07-FEB-1993
DEFINITION H.sapiens mRNA for follicle-stimulating hormone receptor.
ACCESSION X68044
VERSION X68044.1 GI:31473
KEYWORDS follicle stimulating hormone receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 856)
AUTHORS Gromoll,J., Gudermann,T. and Nieschlag,E.
TITLE Molecular cloning of a truncated isoform of the human follicle stimulating hormone receptor
JOURNAL Biochem. Biophys. Res. Commun. 188 (3), 1077-1083 (1992)
PUBMED 1359889
REFERENCE 2
AUTHORS Gromoll,J.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1992) J. Gromoll, Institut f Reproduktionsmedizin, Steinfurter Strasse 107, 4400 Muenster, FRG
FEATURES Location/Qualifiers
source 1. .856
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="testis"
CDS 17. .856
/codon_start=1
/product="follicle stimulating hormone receptor"
/protein_id="CAA48179.1"
/db_xref="GI:31474"
/db_xref="GOA:P23945"
/db_xref="UniProt/Swiss-Prot:P23945"
/translation="MALLLVSLLAFLRLGSGCHHRICHCSNRVFLCQESKVTEIPSDL
PRNAIELRFVLTKLRVIQKGAFSGFGDLEKIEISQNDVLEVIEADVFSNLPKLHEIRI
EKANNLLYINPEAFQNLPNLQYLLISNTGIKHLPDVHKIHSLQKVLLDIQDNINIHTI
ERNSFVGLSFESVILWLNKNGIQEIHNCAFNGTQLDELNLSDNNNLEELPNDVFHGAS
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```
                    NEVV"
ORIGIN

  Query Match            100.0%;  Score 18;  DB 8;  Length 856;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         11 ATAATTATGGCCCTGCTC 28


RESULT 2
S73199
LOCUS       S73199                  1724 bp    DNA     linear   PRI 28-FEB-1995
DEFINITION  follicle-stimulating hormone receptor (5' region) [human, Genomic,
            1724 nt].
ACCESSION   S73199
VERSION     S73199.1  GI:685036
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1724)
  AUTHORS   Gromoll,J., Dankbar,B. and Gudermann,T.
  TITLE     Characterization of the 5' flanking region of the human
            follicle-stimulating hormone receptor gene
  JOURNAL   Mol. Cell. Endocrinol. 102 (1-2), 93-102 (1994)
   PUBMED   7926278
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 155309] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .1724
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            1487. .1642
                     /gene="follicle-stimulating hormone receptor, FSHR"
     CDS             1487. .1642
                     /gene="follicle-stimulating hormone receptor, FSHR"
                     /note="FSHR"
                     /codon_start=1
                     /product="follicle-stimulating hormone receptor"
                     /protein_id="AAB32071.1"
                     /db_xref="GI:685037"
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ORIGIN

  Query Match            100.0%;  Score 18;  DB 8;  Length 1724;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db       1481 ATAATTATGGCCCTGCTC 1498


RESULT 3
HSFSHX1
LOCUS       HSFSHX1                 1734 bp    DNA     linear   PRI 24-JUL-1995
DEFINITION  H.sapiens DNA for follicle stimulating hormone (FSH) receptor.
ACCESSION   Z34260
VERSION     Z34260.1  GI:1052701
KEYWORDS    follicle stimulating hormone receptor; FSH-receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1734)
  AUTHORS   Gromoll,J.
  JOURNAL   Thesis (1994) Institute of Reproductive Medicine, University of
            Muenster
REFERENCE   2  (bases 1 to 1734)
  AUTHORS   Gromoll,J.
  TITLE     Characterization of the 5'-flanking region of the human follicle
            stimulating hormone receptor gene
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1734)
  AUTHORS   Gromoll,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-1994) Gromoll J., University of Muenster
            Institute of Reproductive Medicine Steinfurter Str. 107 Muenster
            Germany 48149
FEATURES             Location/Qualifiers
     source          1. .1734
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /cell_type="Leukocyte"
                     /tissue_type="Blood"
                     /clone_lib="genomic EMBL3"
     exon            1487. .1647
                     /product="FSH receptor"
                     /number=1
     intron          1648. .>1734
                     /number=1
ORIGIN

  Query Match            100.0%;  Score 18;  DB 8;  Length 1734;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db       1481 ATAATTATGGCCCTGCTC 1498


RESULT 4
AR003719
LOCUS       AR003719                2179 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 1 from patent US 5744448.
ACCESSION   AR003719
VERSION     AR003719.1  GI:3964978
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2179)
  AUTHORS   Kelton,C.Ann., Cheng,S.Vui.Yen., Nugent,N.Patrice. and
            Schweickhardt,R.Lynn.
  TITLE     Human follicle stimulating hormone receptor
  JOURNAL   Patent: US 5744448-A 1 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .2179
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            100.0%;  Score 18;  DB 6;  Length 2179;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         69 ATAATTATGGCCCTGCTC 86


RESULT 5
AR067576
LOCUS       AR067576                2179 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5851768.
ACCESSION   AR067576
```

```
VERSION     AR067576.1  GI:5998798
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2179)
  AUTHORS   de la Chapelle,A., Huhtaniemi,I. and Aittomaki,K.
  TITLE     Method for diagnosis of ovarian dysgenesis
  JOURNAL   Patent: US 5851768-A 1 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .2179
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ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 2179;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         69 ATAATTATGGCCCTGCTC 86


RESULT 6
AR207283
LOCUS       AR207283                2179 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 1 from patent US 6372711.
ACCESSION   AR207283
VERSION     AR207283.1  GI:21506147
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2179)
  AUTHORS   Kelton,C.Ann., Cheng,S.Vui.Yen., Nugent,N.Patrice. and
            Schweickhardt,R.Lynn.
  TITLE     Methods for assaying human FSH using human FSH receptor
  JOURNAL   Patent: US 6372711-A 1 16-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .2179
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 2179;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         69 ATAATTATGGCCCTGCTC 86


RESULT 7
S59900
LOCUS       S59900                  2179 bp    mRNA    linear   PRI 23-JUL-1993
DEFINITION  follicle stimulating hormone receptor [human, testis, mRNA, 2179
            nt].
ACCESSION   S59900
VERSION     S59900.1  GI:300072
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2179)
  AUTHORS   Kelton,C.A., Cheng,S.V., Nugent,N.P., Schweickhardt,R.L.,
            Rosenthal,J.L., Overton,S.A., Wands,G.D., Kuzeja,J.B.,
            Luchette,C.A. and Chappel,S.C.
  TITLE     The cloning of the human follicle stimulating hormone receptor and
            its expression in COS-7, CHO, and Y-1 cells
  JOURNAL   Mol. Cell. Endocrinol. 89 (1-2), 141-151 (1992)
  PUBMED    1301382
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 130880] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .2179
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
     gene            1. .2179
                     /gene="follicle stimulating hormone receptor, FSH
                     receptor"
     CDS             75. .2162
                     /gene="follicle stimulating hormone receptor, FSH
                     receptor"
                     /note="FSH receptor"
                     /codon_start=1
                     /product="follicle stimulating hormone receptor"
                     /protein_id="AAB26480.1"
                     /db_xref="GI:300073"
                     /translation="MALLLVSLLAFLSLGSGCHHRICHCSNRVFLCQESKVTEIPSDL
                     PRNAIELRFVLTKLRVIQKGAFSGFGDLEKIEISQNDVLEVIEADVFSNLPKLHEIRI
                     EKANNLLYINPEAFQNLPNLQYLLISNTGIKHLPDVHKIHSLQKVLLDIQDNINIHTI
                     ERNSFVGLSFESVILWLNKNGIQEIHNCAFNGTQLDELNLSDNNNLEELPNDVFHGAS
                     GPVILDISRTRIHSLPSYGLENLKKLRARSTYNLKKLPTLEKLVALMEASLTYPSHCC
                     AFANWRRQISELHPICNKSILRQEVDYMTQTRGQRSSLAEDNESSYSRGFDMTYTEFD
                     YDLCNEVVDVTCSPKPDAFNPCEDIMGYNILRVLIWFISILAITGNIIVLVILTTSQY
                     KLTVPRFLMCNLAFADLCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTV
                     FASELSVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVMGWIFAFAAALFPIFGI
                     SSYMKVSICLPMDIDSPLSQLYVMSLLVLNVLAFVVICGCYIHIYLTVRNPNIVSSSS
                     DTRIAKRMAMLIFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLFHPINSCANPF
                     LYAIFTKNFRRDFFILLSKCGCYEMQAQIYRTETSSTVHNTHPRNGHCSSAPRVTNGS
                     TYILVPLSHLAQN"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 8;  Length 2179;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         69 ATAATTATGGCCCTGCTC 86


RESULT 8
HUMFSHREC
LOCUS       HUMFSHREC               2186 bp    mRNA    linear   PRI 08-NOV-1994
DEFINITION  H.sapiens follicle stimulating hormone receptor mRNA, complete cds.
ACCESSION   M95489
VERSION     M95489.1  GI:182772
KEYWORDS    G-protein coupled receptor; follicle stimulating hormone (FSH)
            receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2186)
  AUTHORS   Tilly,L.T., Aihara,T., Nishimori,K., Jai,X., Billig,H.,
            Kowalski,K.I., Perlas,E.A. and Hsueh,A.J.W.
  TITLE     Expression of recombinant human follicle-stimulating hormone
            receptor: Species-specific ligand binding, signal transduction, and
            identification of multiple ovarian messenger ribonucleic acid
            transcripts
  JOURNAL   Endocrinology (1992) In press
COMMENT     Original source text: Homo sapiens male adult testis cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .2186
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="Unassigned"
                     /sex="male"
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                     /tissue_type="testis"
                     /dev_stage="adult"
     gene            1. .2186
                     /gene="FSHR"
     CDS             76. .2163
                     /gene="FSHR"
                     /codon_start=1
                     /product="follicle stimulating hormone receptor"
                     /protein_id="AAA52478.1"
                     /db_xref="GI:182773"
                     /db_xref="GDB:G00-127-510"
                     /translation="MALLLVSLLAFLSLGSGCHHRICHCSNRVFLCQESKVTEIPSDL
                     PRNAIELRFVLTKLRVIQKGAFSGFGDLEKIEISQNDVLEVIEADVFSNLPKLHEIRI
                     EKANNLLYINPEAFQNLPNLQYLLISNTGIKHLPDVHKIHSLQKVLLDIQDNINIHTI
                     ERNSFVGLSFESVILWLNKNGIQEIHNCAFNGTQLDELNLSDNNNLEELPNDVFHGAS
                     GPVILDISRTRIHSLPSYGLENLKKLRARSTYNLKKLPTLEKLVALMEASLTYPSHCC
                     AFANWRRQISELHPICNKSILRQEVDYMTQTRGQRSSLAEDNESSYSRGFDMTYTEFD
                     YDLCNEVVDVTCSPKPDAFNPCEDIMGYNILRVLIWFISILAITGNIIVLVILTTSQY
                     KLTVPRFLMCNLAFADLCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTV
                     FASELSVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVMGWIFAFAAALFPIFGI
                     SSYMKVSICLPMDIDSPLSQLYVMSLLVLNVLAFVVICGCYIHIYLTVRNPNIVSSSS
                     DTRIAKRMAMLIFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLFHPINSCANPF
                     LYAIFTKNFRRDFFILLSKCGCYEMQAQIYRTETSSTVHNTHPRNGHCSSAPRVTNGS
                     TYILVPLSHLAQN"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 8;  Length 2186;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         70 ATAATTATGGCCCTGCTC 87


RESULT 9
A76125
LOCUS       A76125                 2222 bp    DNA     linear   PAT 19-OCT-1999
DEFINITION  Sequence 1 from Patent WO9320199.
ACCESSION   A76125
VERSION     A76125.1  GI:6088261
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2222)
  AUTHORS   Dijkema,R. and De,L.R.
  TITLE     HUMAN GONADOTROPIN RECEPTOR (FSH RECEPTOR)
  JOURNAL   Patent: WO 9320199-A 1 14-OCT-1993;
            AKZO NV (NL); DIJKEMA REIN (NL)
FEATURES             Location/Qualifiers
     source          1. .2222
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             85. .2172
                     /codon_start=1
                     /evidence=experimental
                     /product="FSH receptor"
                     /protein_id="CAB58589.1"
                     /db_xref="GI:6088262"
                     /translation="MALLLVSLLAFLSLGSGCHHRICHCSNRVFLCQESKVTEIPSDL
                     PRNAIELRFVLTKLRVIQKGAFSGFGDLEKIEISQNDVLEVIEADVFSNLPKLHEIRI
                     EKANNLLYINPEAFQNLPNLQYLLISNTGIKHLPDVHKIHSLQKVLLDIQDNINIHTI
                     ERNSFVGLSFESVILWLNKNGIQEIHNCAFNGTQLDELNLSDNNNLEELPNDVFHGAS
                     GPVILDISRTRIHSLPSYGLENLKKLRARSTYNLKKLPTLEKLVALMEASLTYPSHCC
                     AFANWRRQISELHPICNKSILRQEVDYMTQTRGQRSSLAEDNESSYSRGFDMTYTEFD
                     YDLCNEVVDVTCSPKPDAFNPCEDIMGYNILRVLIWFISILAITGNIIVLVILTTSQY
                     KLTVPRFLMCNLAFADLCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTV
                     FASELSVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVMGWIFAFAAALFPIFGI
                     SSYMKVSICLPMDIDSPLSQLYVMSLLVLNVLAFVVICGCYIHIYLTVRNPNIVSSSS
                     DTRIAKRMAMLIFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLFHPINSCANPF
                     LYAIFTKNFRRDFFILLSKCGCYEMQAQIYRTETSSTVHNTHPRNGHCSSAPRVTNGS
                     TYILVPLSHLAQN"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 2222;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         79 ATAATTATGGCCCTGCTC 96


RESULT 10
CQ715054
LOCUS       CQ715054               2374 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 988 from Patent WO02068579.
ACCESSION   CQ715054
VERSION     CQ715054.1  GI:42275911
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 988 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .2374
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 2374;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         62 ATAATTATGGCCCTGCTC 79


RESULT 11
AR270646
LOCUS       AR270646               2393 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1209 from patent US 6500938.
ACCESSION   AR270646
VERSION     AR270646.1  GI:29701880
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2393)
  AUTHORS   Au-Young,J. and Seilhamer,J.J.
  TITLE     Composition for the detection of signaling pathway gene expression
  JOURNAL   Patent: US 6500938-A 1209 31-DEC-2002;
            Incyte Genomics, Inc.; Palo Alto, CA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .2393
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 2393;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
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  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78


RESULT 12
AX548836
LOCUS       AX548836               2393 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 121 from Patent WO02061087.
ACCESSION   AX548836
VERSION     AX548836.1  GI:25813727
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE     Antigenic peptides, such as for G protein-coupled receptors
            (GPCRs), antibodies thereto, and systems for identifying such
            antigenic peptides
  JOURNAL   Patent: WO 02061087-A 121 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2393
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 2393;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78


RESULT 13
HUMFSHRE
LOCUS       HUMFSHRE               2393 bp    mRNA    linear   PRI 12-JAN-2005
DEFINITION  Human follicle stimulating hormone receptor mRNA, complete cds.
ACCESSION   M65085
VERSION     M65085.1  GI:182770
KEYWORDS    follicle stimulating hormone (FSH) receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2393)
  AUTHORS   Minegishi,T., Nakamura,K., Takakura,Y., Ibuki,Y., Igarashi,M. and
            Minegishi,T.
  TITLE     Cloning and sequencing of human FSH receptor cDNA
  JOURNAL   Biochem. Biophys. Res. Commun. 175 (3), 1125-1130 (1991)
   PUBMED   1709010
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .2393
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="Unassigned"
     gene            1. .2393
                     /gene="FSHR"
     CDS             67. .2154
                     /gene="FSHR"
                     /codon_start=1
                     /product="follicle stimulating hormone receptor"
                     /protein_id="AAA52477.1"
                     /db_xref="GI:182771"
                     /db_xref="GDB:G00-127-510"
                     /translation="MALLLVSLLAFLSLGSGCHHRICHCSNRVFLCQESKVTEIPSDL
                     PRNAIELRFVLTKLRVIQKGAFSGFGDLEKIEISQNDVLEVIEADVFSNLPKLHEIRI
                     EKANNLLYITPEAFQNLPNLQYLLISNTGIKHLPDVHKIHSLQKVLLDIQDNINIHTI
                     ERNSFVGLSFESVILWLNKNGIQEIHNCAFNGTQLDAVNLSDNNNLEELPNDVFHGAS
                     GPVILDISRTRIHSLPSYGLENLKKLRARSTYNLKKLPTLEKLVALMEASLTYPSHCC
                     AFANWRRQISELHPICNKSILRQEVDYMTQARGQRSSLAEDNESSYSRGFDMTYTEFD
                     YDLCNEVVDVTCSPKPDAFNPCEDIMGYNILRVLIWFISILAITGNIIVLVILTTSQY
                     KLTVPRFLMCNLAFADLCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTV
                     FASELSVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVMGWIFAFAAALFPIFGI
                     SSYMKVSICLPMDIDSPLSQLYVMSLLVLNVLAFVVICGCYIHIYLTVRNPNIVSSSS
                     DTRIAKRMAMLIFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLFHPINSCANPF
                     LYAIFTKNFRRDFFILLSKCGCYEMQAQIYRTETSSTVHNTHPRNGHCSSAPRVTSGS
                     TYILVPLSHLAQN"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 8;  Length 2393;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78


RESULT 14
AC092533/c
LOCUS       AC092533               121688 bp    DNA     linear   PRI 15-APR-2005
DEFINITION  Homo sapiens BAC clone RP11-57I10 from 2, complete sequence.
ACCESSION   AC092533 AC027148
VERSION     AC092533.1  GI:14718373
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 121688)
  AUTHORS   Haakenson,W. and Shah,N.
  TITLE     The sequence of Homo sapiens BAC clone RP11-57I10
  JOURNAL   Unpublished (2001)
REFERENCE   2  (bases 1 to 121688)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   3  (bases 1 to 121688)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 121688)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   5  (bases 1 to 121688)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-2005) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Jul 14, 2001 this sequence version replaced gi:7622375.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu
                Contact: submissions@watson.wustl.edu
            -------------- Summary Statistics
```

```
            Center project name: H_NH0057I10
            Drafting Center: WIBR
          --------------.

          NOTICE:

          This sequence was finished as follows unless otherwise noted:
          all regions were double stranded, sequenced with an alternate
          chemistry, or covered by high quality data (i.e., phred quality >=
          30); an attempt was made to resolve all sequencing problems, such
          as compressions and repeats; all regions were covered by sequence
          from more than one subclone; and the assembly was confirmed by
          restriction digest.

          MAPPING INFORMATION:
          Mapping information for this clone was provided by Dr. Wes Warren,
          Department of Genetics, Washington University, St. Louis MO. For
          additional information about the map position of this sequence, see
          http://genome.wustl.edu

          SOURCE INFORMATION:
          The RPCI-11 human BAC library was made from the blood of one male
          donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
          Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
          approach for construction of bacterial artificial chromosome
          libraries. Genomics 51:1-8. The clone may be obtained either from
          Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
          and coworkers at http://www.chori.org
          VECTOR:  pBACe3.6

          NEIGHBORING SEQUENCE INFORMATION:
          The clone sequenced to the left is RP11-125F24, 2000 bp overlap.
          Actual start of this clone is at base position 9748 of RP11-125F24;
          actual end is at base position 121688 of RP11-57I10.

          The sequence of AC027148 has been incorporated into AC092533.
FEATURES             Location/Qualifiers
     source          1. .121688
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /clone="RP11-57I10"
                     /clone_lib="RPCI-11"
     gene            complement(82833. .83058)
                     /gene="FSHR"
     mRNA            complement(82833. .83058)
                     /gene="FSHR"
     CDS             complement(<82833. .82984)
                     /gene="FSHR"
                     /note="Homo sapiens follicle stimulating hormone receptor
                     (FSHR), transcript variant 1, mRNA.; H_NH0057I10.1
                     This gene was based on gi(31657137)
                     Continues as H_NH0125F24.1"
                     /codon_start=1
                     /product="unknown"
                     /protein_id="AAX88895.1"
                     /db_xref="GI:62630150"
                     /translation="MALLLVSLLAFLSLGSGCHHRICHCSNRVFLCQESKVTEIPSDL
                     PRNAIEL"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 8;  Length 121688;
  Best Local Similarity   66.7%;  Pred. No. 5.6;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db      82990 ATAATTATGGCCCTGCTC 82973


RESULT 15
AC083827/c
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```
LOCUS       AC083827              158709 bp    DNA     linear   HTG 24-JAN-2002
DEFINITION  Homo sapiens chromosome 2 clone RP11-345C21, WORKING DRAFT
            SEQUENCE, 23 unordered pieces.
ACCESSION   AC083827
VERSION     AC083827.2  GI:15375221
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 158709)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 158709)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-OCT-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Aug 30, 2001 this sequence version replaced gi:10445290.

            ------------------- Genome Center --------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            Contact: submissions@watson.wustl.edu
            ---------------- Project Information -----------------
            Center project name: H_NH0345C21
            ------------------------------------------------------
            ------------- Summary Statistics  --------------
            Sequencing vector: M13; 100%
            Sequencing vector: plasmid; 0%
            Chemistry: Dye-primer ET; 8% of reads
            Chemistry: Dye-terminator Big Dye; 92% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 142571 bases at least Q40
            Consensus quality: 147681 bases at least Q30
            Consensus quality: 150874 bases at least Q20
            Insert size: 167000; agarose-fp
            Insert size: 156781; sum-of-contigs
            Quality coverage: 3.10 in Q20 bases; agarose-fp
            Quality coverage: 3.36 in Q20 bases; sum-of-contigs
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 23 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1192: contig of 1192 bp in length
            *     1193     1292: gap of unknown length
            *     1293     2772: contig of 1480 bp in length
            *     2773     2872: gap of unknown length
            *     2873     4401: contig of 1529 bp in length
            *     4402     4501: gap of unknown length
            *     4502     6753: contig of 2252 bp in length
            *     6754     6853: gap of unknown length
            *     6854     8763: contig of 1910 bp in length
            *     8764     8863: gap of unknown length
            *     8864    11063: contig of 2200 bp in length
            *    11064    11163: gap of unknown length
            *    11164    14152: contig of 2989 bp in length
            *    14153    14252: gap of unknown length
            *    14253    17321: contig of 3069 bp in length
            *    17322    17421: gap of unknown length
            *    17422    19872: contig of 2451 bp in length
            *    19873    19972: gap of unknown length
            *    19973    22886: contig of 2914 bp in length
            *    22887    22986: gap of unknown length
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            *    22987    26989: contig of 4003 bp in length
            *    26990    27089: gap of unknown length
            *    27090    31373: contig of 4284 bp in length
            *    31374    31473: gap of unknown length
            *    31474    36312: contig of 4839 bp in length
            *    36313    36412: gap of unknown length
            *    36413    41598: contig of 5186 bp in length
            *    41599    41698: gap of unknown length
            *    41699    49543: contig of 7845 bp in length
            *    49544    49643: gap of unknown length
            *    49644    56734: contig of 7091 bp in length
            *    56735    56834: gap of unknown length
            *    56835    66438: contig of 9604 bp in length
            *    66439    66538: gap of unknown length
            *    66539    76934: contig of 10396 bp in length
            *    76935    77034: gap of unknown length
            *    77035    88008: contig of 10974 bp in length
            *    88009    88108: gap of unknown length
            *    88109   101914: contig of 13806 bp in length
            *   101915   102014: gap of unknown length
            *   102015   117937: contig of 15923 bp in length
            *   117938   118037: gap of unknown length
            *   118038   133609: contig of 15572 bp in length
            *   133610   133709: gap of unknown length
            *   133710   158709: contig of 25000 bp in length.
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                     /db_xref="taxon:9606"
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                     /clone="RP11-345C21"
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     gap             2773. .2872
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     misc_feature    2873. .4401
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     gap             4402. .4501
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     misc_feature    4502. .6753
                     /note="assembly_name:Contig9"
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     misc_feature    8864. .11063
                     /note="assembly_name:Contig11"
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     misc_feature    11164. .14152
                     /note="assembly_name:Contig12"
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     misc_feature    17422. .19872
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                     /estimated_length=unknown
     misc_feature    19973. .22886
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     misc_feature    27090. .31373
                     /note="assembly_name:Contig17"
     gap             31374. .31473
                     /estimated_length=unknown
     misc_feature    31474. .36312
                     /note="assembly_name:Contig18"
     gap             36313. .36412
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     misc_feature    36413. .41598
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     gap             56735. .56834
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     misc_feature    56835. .66438
                     /note="assembly_name:Contig22"
     gap             66439. .66538
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     misc_feature    66539. .76934
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     misc_feature    88109. .101914
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     gap             101915. .102014
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     misc_feature    118038. .133609
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ORIGIN

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Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db      35257 ATAATTATGGCCCTGCTC 35240


Search completed: November 29, 2005, 23:42:25
Job time : 895.5 secs
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 18:22:32 ; Search time 223.5 Seconds
(without alignments)
536.754 Million cell updates/sec

Title: US-10-018-716B-2
Perfect score: 18
Sequence: 1 auaauuauggcccugcuc 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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8: geneseqn2003as:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	18	100.0	18	4	AAC90409	Aac90409 Human FSH
c	2	18	100.0	18	4	AAC90408	Aac90408 Human FSH
	3	18	100.0	1922	11	ADP03559	Adp03559 Human GPC
	4	18	100.0	2019	10	ADC24202	Adc24202 Human NOV
	5	18	100.0	2179	2	AAT63181	Aat63181 FSH recep
	6	18	100.0	2180	2	AAQ29377	Aaq29377 FSHR DNA.
	7	18	100.0	2222	2	AAQ50013	Aaq50013 FSH recep
	8	18	100.0	2393	8	ABZ42665	Abz42665 Human fol
	9	18	100.0	2393	10	ADD25503	Add25503 Binding d
	10	18	100.0	2393	10	ACA56611	Aca56611 Human sig
	11	18	100.0	2393	12	ADI56407	Adi56407 Human pol
	12	18	100.0	2393	12	ADO29879	Ado29879 Human GPC
c	13	15	83.3	507	13	ADR26224	Adr26224 Breast ca
	14	15	83.3	612	6	ABT03390	Abt03390 Ovary cel
	15	15	83.3	628	6	ABT03391	Abt03391 Ovary cel
c	16	15	83.3	2021	13	ADT19293	Adt19293 Plant cDN
	17	15	83.3	3659	4	ABL12007	Abl12007 Drosophil
c	18	15	83.3	8253	13	ADR84405	Adr84405 Aspergill
	19	15	83.3	9140	4	ABL12006	Abl12006 Drosophil
c	20	15	83.3	76829	14	AEA61117	Aea61117 Human FLJ
	21	15	83.3	180227	13	ABD33268	Abd33268 Human can
	22	15	83.3	202251	11	ACN44504	Acn44504 Mouse gen
c	23	14	77.8	400	14	AEB67475	Aeb67475 Rice geno
c	24	14	77.8	574	11	ADT97777	Adt97777 Colon can
c	25	14	77.8	574	11	ADX44259	Adx44259 Human cDN
c	26	14	77.8	810	8	ACA36201	Aca36201 Prokaryot
	27	14	77.8	900	11	ABD01221	Abd01221 Klebsiell
	28	14	77.8	975	13	ADT45042	Adt45042 Bacterial
	29	14	77.8	1059	5	AAH65707	Aah65707 C glutami
	30	14	77.8	1149	4	AAF67932	Aaf67932 Corynebac
	31	14	77.8	1200	14	ADZ62987	Adz62987 Murine Hs
	32	14	77.8	1254	13	ADS59283	Ads59283 Bacterial
c	33	14	77.8	1506	13	ADS48503	Ads48503 Bacterial
c	34	14	77.8	1617	5	AAS93640	Aas93640 DNA encod
c	35	14	77.8	1887	4	AAI58166	Aai58166 Human pol
c	36	14	77.8	1887	5	ADQ98372	Adq98372 DNA encod
c	37	14	77.8	1887	9	ADB48132	Adb48132 Novel hum
c	38	14	77.8	1887	13	ADS47940	Ads47940 Bacterial
c	39	14	77.8	1903	4	AAH17958	Aah17958 Human cDN
	40	14	77.8	2450	10	ADB68874	Adb68874 C. neofor
	41	14	77.8	2975	6	AAD29106	Aad29106 Human MDM
	42	14	77.8	3678	2	AAQ53996	Aaq53996 Equine he
	43	14	77.8	3678	2	AAX38299	Aax38299 Equine he
c	44	14	77.8	3762	11	ACH99131	Ach99131 Klebsiell
c	45	14	77.8	4262	2	AAT38484	Aat38484 Rat petri

ALIGNMENTS

RESULT 1
AAC90409
ID AAC90409 standard; RNA; 18 BP.
XX
AC AAC90409;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human FSH receptor specific antisense oligonucleotide #2.
XX
KW Human; cytostatic; follicle-stimulating hormone receptor; FSHR;
KW fertility; menstrual cycle; chemopreventive; chemotherapy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200073416-A1.
XX
PD 07-DEC-2000.
XX
PF 16-MAY-2000; 2000WO-US013488.
XX
PR 28-MAY-1999; 99US-0136489P.
PR 08-OCT-1999; 99US-0158612P.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Labarbera AR, Zhu C, Wang Y;
XX
DR WPI; 2001-091069/10.
XX
PT New composition for regulating fertility, and for chemoprevention and
PT chemotherapy of cancer, comprises an antisense oligonucleotide that is
PT complementary to a nucleotide sequence of a follicle-stimulating hormone
PT receptor.
XX
PS Claim 13; Page 29; 89pp; English.
XX
CC The present invention relates to a composition, which comprises at least
CC one antisense oligonucleotide that is complementary to follicle-
CC stimulating hormone receptor (FSHR) coding sequence. The present sequence
CC is one such oligonucleotide used in the composition. The composition of
CC the present invention can be used for regulating hormones of a host. The

```
CC   composition is also useful for regulating fertility and menstrual cycle.
CC   In addition, the composition is useful as a chemopreventive or
CC   chemotherapy for cancers (e.g. breast, bladder, cervix, lung, liver,
CC   ovary, colon, stomach, or especially ovarian cancers), gestational
CC   trophoblastic tumours or testicular germ cell tumours
XX
SQ   Sequence 18 BP; 4 A; 5 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              ||||||||||||||||||
Db          1 AUAAUUAUGGCCCUGCUC 18


RESULT 2
AAC90408/c
ID   AAC90408 standard; DNA; 18 BP.
XX
AC   AAC90408;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human FSH receptor specific antisense oligonucleotide #1.
XX
KW   Human; cytostatic; follicle-stimulating hormone receptor; FSHR;
KW   fertility; menstrual cycle; chemopreventive; chemotherapy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073416-A1.
XX
PD   07-DEC-2000.
XX
PF   16-MAY-2000; 2000WO-US013488.
XX
PR   28-MAY-1999;   99US-0136489P.
PR   08-OCT-1999;   99US-0158612P.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Labarbera AR,  Zhu C,  Wang Y;
XX
DR   WPI; 2001-091069/10.
XX
PT   New composition for regulating fertility, and for chemoprevention and
PT   chemotherapy of cancer, comprises an antisense oligonucleotide that is
PT   complementary to a nucleotide sequence of a follicle-stimulating hormone
PT   receptor.
XX
PS   Claim 13; Page 29; 89pp; English.
XX
CC   The present invention relates to a composition, which comprises at least
CC   one antisense oligonucleotide that is complementary to follicle-
CC   stimulating hormone receptor (FSHR) coding sequence. The present sequence
CC   is one such oligonucleotide used in the composition. The composition of
CC   the present invention can be used for regulating hormones of a host. The
CC   composition is also useful for regulating fertility and menstrual cycle.
CC   In addition, the composition is useful as a chemopreventive or
CC   chemotherapy for cancers (e.g. breast, bladder, cervix, lung, liver,
CC   ovary, colon, stomach, or especially ovarian cancers), gestational
CC   trophoblastic tumours or testicular germ cell tumours
XX
SQ   Sequence 18 BP; 6 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

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  Best Local Similarity   66.7%;  Pred. No. 1.2;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db          1 ATAATTATGGCCCTGCTC 18


RESULT 3
ADP03559
ID   ADP03559 standard; DNA; 1922 BP.
XX
AC   ADP03559;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human GPCR follicle stimulating hormone receptor variant "Gene 4" DNA.
XX
KW   GPCR; G-protein coupled receptor; neuroprotective; nootropic;
KW   tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant;
KW   anticonvulsant; antiparkinsonian; cytostatic; cardiant; hypotensive;
KW   antianginal; analgesic; anorectic; anti-HIV; antiasthmatic; osteopathic;
KW   uropathic; antiulcer; antiallergic; cell cycle regulation; neurological;
KW   severe mental retardation; dyskinesia; brain; spinal cord; affective;
KW   neoplastic; cardiovascular; immunological; immune; endocrinal; growth;
KW   eating; HIV infection; cancer; metabolic; pituitary;
KW   chromosome identification; gene therapy; human; ds; gene;
KW   follicle stimulating hormone; FSH receptor variant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             17. .1753
FT                   /*tag=  a
FT                   /product= "Human GPCR follicle stimulating hormone
FT                   receptor variant "Gene 4" protein"
XX
PN   WO2003062393-A2.
XX
PD   31-JUL-2003.
XX
PF   22-JAN-2003; 2003WO-US001911.
XX
PR   22-JAN-2002; 2002US-0350724P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Ramanathan CS,  Gopal S,  Mintier G,  Feder JN;
XX
DR   WPI; 2003-618283/58.
DR   P-PSDB; ADP03570.
XX
PT   New nucleic acid molecule encoding a human G-protein coupled receptor,
PT   useful for diagnosing, preventing or treating diseases involving the
PT   receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
PT   cancer.
XX
PS   Claim 1; SEQ ID NO 4; 224pp; English.
XX
CC   The invention relates to a novel isolated GPCR (G-protein coupled
CC   receptor) nucleic acid molecule. The polynucleotide and polypeptide of
CC   the invention demonstrate neuroprotective, nootropic, tranquiliser,
CC   antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,
CC   antiparkinsonian, cytostatic, cardiant, hypotensive, antianginal,
CC   analgesic, anorectic, anti-HIV, antiasthmatic, osteopathic, uropathic,
CC   antiulcer and antiallergic properties. The nucleic acid molecule and
CC   polypeptide of the invention may be useful in diagnosing, preventing,
CC   treating or ameliorating a medical condition, such as a disorder related
CC   to aberrant G-protein coupled signalling, a disorder related to aberrant
CC   cell cycle regulation, neurological disorders, severe mental retardation
CC   and dyskinesias, brain disorders, spinal cord disorders, affective
CC   disorders, neoplastic disorders, cardiovascular disorders, immunological
CC   disorders, immune-related disorders, endocrinal diseases, growth
CC   disorders, eating disorders, HIV infection, cancers, metabolic disorders
CC   and pituitary disorders. Furthermore, the polynucleotide may be used in
CC   chromosome identification, in identifying organisms from minute
CC   biological samples, in gene therapy or as a molecular weight marker. The
CC   current sequence is that of a human GPCR (G-protein coupled receptor) DNA
```

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CC   which was isolated by the method of the invention.
XX
SQ   Sequence 1922 BP; 499 A; 504 C; 387 G; 532 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 11;  Length 1922;
  Best Local Similarity   66.7%;  Pred. No. 1.3;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         11 ATAATTATGGCCCTGCTC 28


RESULT 4
ADC24202
ID   ADC24202 standard; cDNA; 2019 BP.
XX
AC   ADC24202;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human NOV3a encoding cDNA SEQ ID NO:9.
XX
KW   human; NOVX; cardiant; antiarteriosclerotic; hypotensive; vasotropic;
KW   dermatological; anorectic; immunosuppressive; cytostatic;
KW   antiinfertility; haemostatic; anti-HIV; antiasthmatic; antiinflammatory;
KW   neuroprotective; anabolic; nootropic; antiparkinsonian; gene therapy;
KW   cardiomyopathy; atherosclerosis; hypertension; congenital heart defect;
KW   pulmonary stenosis; scleroderma; obesity; metabolic disturbance; obesity;
KW   transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;
KW   prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma;
KW   fertility; haemophilia; graft versus host disease; AIDS;
KW   bronchial asthma; Crohn's disease; multiple sclerosis;
KW   infectious disease; anorexia; neurodegenerative disorder;
KW   Alzheimer's disease; Parkinson's disease; immune disorder;
KW   haematopoietic disorder; dyslipidaemia; wasting disorder; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             61. .1962
FT                   /*tag=  a
FT                   /product= "NOV3a"
XX
PN   WO2003076584-A2.
XX
PD   18-SEP-2003.
XX
PF   06-MAR-2003; 2003WO-US006951.
XX
PR   06-MAR-2002; 2002US-0361974P.
PR   19-MAR-2002; 2002US-0365477P.
PR   22-MAR-2002; 2002US-0366928P.
PR   06-AUG-2002; 2002US-0401661P.
PR   05-MAR-2003; 2003US-00401661.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Alsobrook JP,  Burgess CE,  Edinger SR,  Gerlach VL,  Ji W,  Kekuda R;
PI   Li L,  Macdougall JR,  Miller CE,  Millet I,  Patturajan M,  Pena CEA;
PI   Rieger DK,  Sciore P,  Shenoy SG,  Smithson G,  Spytek KA,  Stone DJ;
PI   Voss EZ,  Zhong M;
XX
DR   WPI; 2003-722330/68.
DR   P-PSDB; ADC24203.
XX
PT   New NOVX polypeptides and nucleic acids, useful for diagnosing or
PT   treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma,
PT   obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or
PT   multiple sclerosis.
XX
PS   Claim 20; SEQ ID NO 9; 229pp; English.
XX
CC   The present invention describes novel human proteins, designated NOVX
CC   proteins. The NOVX sequences have cardiant, antiarteriosclerotic,
CC   hypotensive, vasotropic, dermatological, anorectic, immunosuppressive,
CC   cytostatic, antiinfertility, haemostatic, anti-HIV, antiasthmatic,
CC   antiinflammatory, neuroprotective, anabolic, nootropic and
CC   antiparkinsonian activities, and can be used in gene therapy. The NOVX
CC   sequences can be used as a therapeutic in the manufacture of a medicament
CC   for treating a syndrome associated with a human disease, such as a
CC   pathology associated with NOVX. The NOVX proteins and nucleic acids
CC   encoding them are useful for diagnosing or treating pathologies, diseases
CC   or conditions associated with NOVX sequences, including cardiomyopathy,
CC   atherosclerosis, hypertension, congenital heart defects, pulmonary
CC   stenosis, scleroderma, obesity, metabolic disturbances associated with
CC   obesity, transplantation, adrenoleukodystrophy, congenital adrenal
CC   hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm,
CC   adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,
CC   bronchial asthma, Crohn's disease, multiple sclerosis, infectious
CC   disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,
CC   or Parkinson's disease), immune disorders, haematopoietic disorders,
CC   dyslipidaemias, and wasting disorders associated with chronic diseases.
CC   The proteins can also be used as immunogens to produce antibodies and as
CC   vaccines. The sequences may further be used in chromosome mapping,
CC   identifying individual from minute biological samples (tissue typing),
CC   and in forensic identification of a biological sample. The present
CC   sequence encodes human NOV3a from the present invention.
XX
SQ   Sequence 2019 BP; 527 A; 514 C; 411 G; 567 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 10;  Length 2019;
  Best Local Similarity   66.7%;  Pred. No. 1.3;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         55 ATAATTATGGCCCTGCTC 72


RESULT 5
AAT63181
ID   AAT63181 standard; DNA; 2179 BP.
XX
AC   AAT63181;
XX
DT   20-JUN-1997  (first entry)
XX
DE   FSH receptor gene wild-type allele.
XX
KW   Follicle stimulating hormone receptor; FSH receptor; ovarian dysgenesis;
KW   hypergonadotropic hypogonadism; diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            70. .227
FT                   /*tag=  c
FT                   /note= "nucleotides 70-227 correspond to nucleotides 1-
FT                   158 of fshr exon 1"
FT   CDS             75. .2159
FT                   /*tag=  a
FT   exon            228. .298
FT                   /*tag=  c
FT                   /note= "nucleotides 228-298 correspond to nucleotides 7-
FT                   77 of fshr exon 2"
FT   exon            299. .373
FT                   /*tag=  c
FT                   /note= "nucleotides 299-373 correspond to nucleotides 6-
FT                   80 of fshr exon 3"
FT   exon            374. .450
FT                   /*tag=  c
FT                   /note= "nucleotides 374-450 correspond to nucleotides 6-
FT                   82 of fshr exon 4"
FT   exon            451. .520
FT                   /*tag=  c
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```
FT                   /note= "nucleotides 451-520 correspond to nucleotides 8-
FT                   77 of fshr exon 5"
FT   exon            521. .598
FT                   /*tag=  c
FT                   /note= "nucleotides 521. .598 correspond to nucleotides 6-
FT                   83 of fshr exon 6"
FT   exon            599. .668
FT                   /*tag=  c
FT                   /note= "nucleotides 599-668 correspond to nucleotides 6-
FT                   75 of fshr exon 7"
FT   mutation        640
FT                   /*tag=  b
FT                   /note= "a C to T mutation in codon 189 correlates with
FT                   ovarian dysgenesis"
FT   exon            669. .742
FT                   /*tag=  c
FT                   /note= "nucleotides 669-742 correspond to nucleotides 7-
FT                   80 of fshr exon 8"
FT   exon            743. .928
FT                   /*tag=  c
FT                   /note= "nucleotides 743-928 correspond to nucleotides 6-
FT                   191 of fshr exon 9"
FT   exon            929. .2179
FT                   /*tag=  c
FT                   /note= "nucleotides 929-2179 correspond to nucleotides
FT                   102-1352 of fshr exon 10"
XX
PN   WO9711194-A1.
XX
PD   27-MAR-1997.
XX
PF   20-SEP-1996;   96WO-FI000501.
XX
PR   20-SEP-1995;   95US-00531070.
XX
PA   (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI   De La Chapelle A,  Aittomaeki K,  Huhtaniemi I;
XX
DR   WPI; 1997-202900/18.
DR   P-PSDB; AAW14782.
XX
PT   Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities - by
PT   amplifying DNA including follicle stimulating hormone receptor allele(s),
PT   i.e. codon 189, cleaving fragments, and examination.
XX
PS   Claim 17; Page 18-21; 43pp; English.
XX
CC   A DNA sequence (AAT63181) comprises the coding region from exons 1-10 of
CC   the wild-type fshr gene that codes for human follicle stimulating hormone
CC   (FSH) receptor (AAW14782). A C to T mutation in exon 7 (codon 189) is
CC   associated with ovarian dysgenesis. In a method for determining a FSH
CC   receptor genotype in a human patient, fshr exon 7, or a portion of it, is
CC   isolated by PCR amplification (see also AAT63195-96) and exposed to BsmI.
CC   Exon 7 contains a unique BsmI site which, if mutated, will produce no
CC   BsmI digestion products, thereby enabling diagnosis of ovarian dysgenesis
XX
SQ   Sequence 2179 BP; 575 A; 561 C; 444 G; 599 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 2;  Length 2179;
  Best Local Similarity   66.7%;  Pred. No. 1.3;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         69 ATAATTATGGCCCTGCTC 86


RESULT 6
AAQ29377
ID   AAQ29377 standard; DNA; 2180 BP.
XX
AC   AAQ29377;
XX
DT   25-MAR-2003  (revised)
DT   04-MAR-1993  (first entry)
XX
DE   FSHR DNA.
XX
KW   Human; follicle stimulating hormone receptor; maturation;
KW   spermatogenesis; birth control; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             75. .2159
FT                   /*tag=  a
FT   sig_peptide     75. .126
FT                   /*tag=  b
FT   mat_peptide     127. .2159
FT                   /*tag=  c
XX
PN   WO9216620-A1.
XX
PD   01-OCT-1992.
XX
PF   02-JAN-1992;   92WO-US000122.
XX
PR   15-MAR-1991;   91US-00670085.
XX
PA   (ISTF ) ARS APPL RES SYST HOLDING NV.
XX
PI   Kelton CA,  Cheng SVY,  Nugent NP,  Schweickhardt RL;
XX
DR   WPI; 1992-349206/42.
DR   P-PSDB; AAR29377.
XX
PT   Pure human FSH receptor, fragments and mutants - for preventing follicle
PT   growth, maturation and spermatogenesis, also for use of appropriate cell
PT   lines for bio-assays of FSH.
XX
PS   Claim 7; Page 25; 48pp; English.
XX
CC   The DNA sequence encoding human follicle stimulating hormone receptor
CC   (FSHR) was obtd. by screening a lambda gt11 cDNA library constructed from
CC   RNA extracted from human testis and amplified, with a rat FSHR cDNA clone
CC   as a probe. Positive colonies were used for a secondary screen which
CC   isolated five putative human FSHR clones. None of the clones contained
CC   the complete hFSHR coding region but could be overlapped using GCG to
CC   give the complete sequence. hFSHR binds to FSH to reduce endogenous FSH
CC   bioactivity, in females to prevent follicle growth and maturation and in
CC   males to prevent spermatogenesis, i.e. as a birth control agent. (Updated
CC   on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2180 BP; 577 A; 560 C; 444 G; 599 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 2;  Length 2180;
  Best Local Similarity   66.7%;  Pred. No. 1.3;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         70 ATAATTATGGCCCTGCTC 87


RESULT 7
AAQ50013
ID   AAQ50013 standard; cDNA to mRNA; 2222 BP.
XX
AC   AAQ50013;
XX
DT   25-MAR-2003  (revised)
DT   05-MAY-1994  (first entry)
XX
DE   FSH receptor.
XX
```

```
KW   FSH; receptor; follicle stimulating hormone; GST;
KW   glutathione-S-transferase; primer; PCR; amplification;
KW   polymerase chain reaction; probe; antibody; overstimulation; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             85. .2172
FT                   /*tag= a
FT                   /product= "FSH_receptor"
FT   primer_bind     136. .151
FT                   /*tag= b
FT                   /note= "first primer for GST-FSH-R1 and for GST-FSH-R2"
FT   primer_bind     763. .776
FT                   /*tag= d
FT                   /note= "primer for GST-FSH-R3"
FT   primer_bind     complement(770. .787)
FT                   /*tag= f
FT                   /note= "primer for GST-FSH-R2"
FT   primer_bind     complement(1167. .1183)
FT                   /*tag= e
FT                   /note= "primer for GST-FSH-R1 and for GST-FSH-R3"
FT   primer_bind     1168. .1183
FT                   /*tag= c
FT                   /note= "primer for GST-FSH-R3"
XX
PN   WO9320199-A1.
XX
PD   14-OCT-1993.
XX
PF   29-MAR-1993;   93WO-EP000780.
XX
PR   30-MAR-1992;   92EP-00200886.
XX
PA   (ALKU ) AKZO NV.
XX
PI   Dijkema R,  De Leeuw R;
XX
DR   WPI; 1993-336907/42.
DR   P-PSDB; AAR42082.
XX
PT   New follicle stimulating hormone receptor - and derived antibodies, anti-
PT   idiotypic antibodies, and transfected cells, useful e.g. in diagnosis and
PT   as antidote for FSH overstimulation.
XX
PS   Disclosure; Page 20-23; 42pp; English.
XX
CC   The primers given in AAQ50029-34 were used in the cloning of GST-FSH- R1,
CC   GST-FSH-R2 and GST-FSH-R3 fusion protein constructs. Screening of the
CC   human testis cDNA library with a hFSH-R specific probe resulted in five
CC   recombinant phages positive in hybridisation. Sequence analysis was
CC   performed of the 2222 bp fragment of pGEM3Zc1 (AAQ50013). (Updated on 25-
CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 2222 BP; 598 A; 565 C; 453 G; 606 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 2;  Length 2222;
  Best Local Similarity   66.7%;  Pred. No. 1.3;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         79 ATAATTATGGCCCTGCTC 96


RESULT 8
ABZ42665
ID   ABZ42665 standard; DNA; 2393 BP.
XX
AC   ABZ42665;
XX
DT   04-MAR-2003  (first entry)
XX
DE   Human follicle stimulating hormone receptor nucleotide SEQ ID NO:121.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200261087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
XX
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC,  Roush CL,  Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   P-PSDB; ABP81819.
XX
PT   New isolated antigenic peptides e.g., for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 1; 523pp; English.
XX
CC   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific
CC   antibodies. The peptides and antibodies are also useful for detecting the
CC   presence or absence of corresponding GPCRs. The antigenic peptides for
CC   GPCRs and antibodies are useful for diagnosing and designing drugs for
CC   treating immune-related diseases, growth-related diseases, cell
CC   regeneration-related disease, immunological-related cell proliferative
CC   diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC   atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC   osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC   inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC   disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC   anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC   loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC   hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC   any other disorder in which GPCRs are involved. The antibodies may be
CC   used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 8;  Length 2393;
  Best Local Similarity   66.7%;  Pred. No. 1.3;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78
```

```
RESULT 9
ADD25503
ID   ADD25503 standard; DNA; 2393 BP.
XX
AC   ADD25503;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Binding domain-immunoglobulin fusion protein-associated DNA #36.
XX
KW   ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW   antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW   neuroprotective; hinge region; immunoglobulin heavy chain;
KW   CH2 constant region; CH3 constant region; IgG1;
KW   antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW   malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW   rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW   type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS   Unidentified.
XX
PN   US2003118592-A1.
XX
PD   26-JUN-2003.
XX
PF   25-JUL-2002; 2002US-00207655.
XX
PR   17-JAN-2001; 2001US-0367358P.
PR   17-JAN-2002; 2002US-00053530.
PR   03-JUN-2002; 2002US-0385691P.
XX
PA   (GENE-) GENECRAFT INC.
XX
PI   Ledbetter JA,  Hayden-Ledbetter MS,  Thompson PA;
XX
DR   WPI; 2003-801317/75.
XX
PT   New binding domain-immunoglobulin fusion protein, useful for treating a
PT   subject having or suspected of having a malignant condition or a B-cell
PT   disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS   Disclosure; SEQ ID NO 64; 157pp; English.
XX
CC   Unidentified
XX
SQ   Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 10;  Length 2393;
  Best Local Similarity   66.7%;  Pred. No. 1.3;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78


RESULT 10
ACA56611
ID   ACA56611 standard; cDNA; 2393 BP.
XX
AC   ACA56611;
XX
DT   06-JUN-2003  (first entry)
XX
DE   Human signalling pathway polynucleotide probe SEQ ID NO 1209.
XX
KW   Human; probe; ss; array element; Parkinson's disease;
KW   signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW   immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS   Homo sapiens.
XX
PN   US6500938-B1.
XX
PD   31-DEC-2002.
XX
PF   30-JAN-1998;   98US-00016434.
XX
PR   30-JAN-1998;   98US-00016434.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Au-Young J,  Seilhamer JJ;
XX
DR   WPI; 2003-352189/33.
XX
PT   Combination of polynucleotide probes, useful as array elements in a
PT   microarray for monitoring the expression of a number of target
PT   polynucleotides.
XX
PS   Claim 1; SEQ ID NO 1209; 65pp; English.
XX
CC   The invention relates to a combination which, comprises a number of
CC   polynucleotide probes comprising a sequence selected from one of the 1490
CC   sequences mentioned in the specification. The combination is useful as an
CC   array element in a microarray for monitoring the expression of a number
CC   of target polynucleotides. The microarray is particularly useful in the
CC   diagnosis and treatment of cancer and immunopathology and neuropathology.
CC   The microarray is useful in diagnostics and treatment regimens, drug
CC   discovery and development, toxicological and carcinogenicity studies,
CC   forensics and pharmacogenomics. The microarray is also useful for
CC   monitoring progression of diseases and for developing sophisticated
CC   profiles for the effects of currently available therapeutic drugs. The
CC   combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC   and genomic fragments and in research and diagnostic applications. The
CC   array can detect changes in expression in a large number of genes coding
CC   for different signaling pathway populations which can be used to diagnose
CC   various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC   immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC   and Parkinson's disease. The present sequence represents a polynucleotide
CC   probe of the invention. Note: The sequence data for this patent did not
CC   form part of the printed specification but was obtained in electronic
CC   format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ   Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 10;  Length 2393;
  Best Local Similarity   66.7%;  Pred. No. 1.3;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78


RESULT 11
ADI56407
ID   ADI56407 standard; DNA; 2393 BP.
XX
AC   ADI56407;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human polynucleotide probe #1209.
XX
KW   Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
KW   effector-like polypeptide; cancer; immunopathology; neuropathology;
KW   drug development; toxicology; carcinogenicity;
KW   signalling pathway polypeptide; adrenal gland; bladder; bone;
KW   bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW   diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW   dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX
```

OS Homo sapiens.
XX
PN US2004010136-A1.
XX
PD 15-JAN-2004.
XX
PF 26-NOV-2002; 2002US-00305720.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2004-090520/09.
XX
PT New composition comprising polynucleotide probes, useful as array
PT elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.
XX
PS Claim 6; SEQ ID NO 1209; 73pp; English.
XX
CC The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC polypeptide and third polynucleotide probes comprising at least a portion
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray is useful in the
CC diagnosis and treatment of cancer, an immunopathology or a
CC neuropathology. It can also be used for drug discovery and development,
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC Microarrays can also be used for monitoring the progression of diseases
CC that may be associated with the altered expression of signalling pathway
CC polypeptides. The composition can also be used to purify a subpopulation
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC epilepsy, Alzheimer's disease or depression. This sequence represents a
CC human polynucleotide probe of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 2393;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 12; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78
```

RESULT 12
ADO29879
ID ADO29879 standard; cDNA; 2393 BP.
XX
AC ADO29879;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human GPCR FSHR polynucleotide, SEQ ID NO:981.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX
PA (PRIM-) PRIMAL INC.
XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
DR WPI; 2004-390329/36.
DR P-PSDB; ADO29321.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 151; SEQ ID NO 981; 542pp; English.
XX
CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the trasngenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 2393;

```
  Best Local Similarity   66.7%;  Pred. No. 1.3;
  Matches   12;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AUAAUUAUGGCCCUGCUC 18
              |:||::|:|||||:||:|
Db         61 ATAATTATGGCCCTGCTC 78


RESULT 13
ADR26224/c
ID   ADR26224 standard; DNA; 507 BP.
XX
AC   ADR26224;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Breast cancer prognosis marker #2085.
XX
KW   ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2004065545-A2.
XX
PD   05-AUG-2004.
XX
PF   15-JAN-2004; 2004WO-US001100.
XX
PR   15-JAN-2003; 2003US-00342887.
XX
PA   (ROSE-) ROSETTA INPHARMATICS LLC.
PA   (NECA-) NETHERLANDS CANCER INST.
XX
PI   Van't Veer LJ,  He Y;
XX
DR   WPI; 2004-593473/57.
XX
PT   Classifying a breast cancer patient according to prognosis comprises
PT   determining the similarity between the level of expression of each of
PT   five genes in a cell sample taken from patient, to control levels.
XX
PS   Disclosure; SEQ ID NO 2085; 226pp; English.
XX
CC   The invention relates to a method of classifying a breast cancer patient
CC   according to prognosis by determining the similarity between the level of
CC   expression of each of five genes for which markers are listed in the
CC   specification, in a cell sample taken from the breast cancer patient, to
CC   control levels of expression for each respective five genes to obtain a
CC   patient similarity value. The methods are useful for classifying a breast
CC   cancer patient according to prognosis. Kits and computer program products
CC   are useful for data analysis using the diagnostic, prognostic and
CC   statistical methods of the invention. This sequence corresponds to a
CC   marker used in the method of the invention.
XX
SQ   Sequence 507 BP; 151 A; 103 C; 90 G; 163 T; 0 U; 0 Other;

  Query Match             83.3%;  Score 15;  DB 13;  Length 507;
  Best Local Similarity   66.7%;  Pred. No. 64;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAUUAUGGCCCUGCU 17
              ||::|:|||||:||:
Db        177 AATTATGGCCCTGCT 163


RESULT 14
ABT03390
ID   ABT03390 standard; DNA; 612 BP.
XX
AC   ABT03390;
XX
DT   28-NOV-2002  (first entry)
XX
DE   Ovary cell-specific DNA sequence 106.
XX
KW   Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
KW   ovary specific protein; ovarian cancer; breast cancer; ss; vaccine;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200238606-A2.
XX
PD   16-MAY-2002.
XX
PF   07-NOV-2001; 2001WO-US046459.
XX
PR   08-NOV-2000; 2000US-0246640P.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Sun Y,  Recipon H,  Salceda S,  Liu C;
XX
DR   WPI; 2002-519297/55.
XX
PT   Polypeptide and polynucleotides present in normal and neoplastic ovary
PT   cells, useful for identifying, monitoring, staging, diagnosing,
PT   preventing and treating ovarian cancer, and non-cancerous disease states
PT   in the ovary.
XX
PS   Claim 1; Page 192; 247pp; English.
XX
CC   The invention comprises amino acid and DNA sequences which are present in
CC   normal and neoplastic ovary cells. The DNA and protein sequences of the
CC   invention are useful for determining the presence of an ovary specific
CC   nucleic acid or an ovary specific protein in a sample. The DNA and
CC   protein sequences of the invention are useful for diagnosing and
CC   monitoring the presence and metastasis of ovarian cancer and breast
CC   cancer. Nucleotides ABT03285 - ABT03421 represents the ovary cell
CC   specific DNA sequences of the invention
XX
SQ   Sequence 612 BP; 202 A; 112 C; 108 G; 190 T; 0 U; 0 Other;

  Query Match             83.3%;  Score 15;  DB 6;  Length 612;
  Best Local Similarity   66.7%;  Pred. No. 64;
  Matches   10;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 AAUUAUGGCCCUGCU 17
              ||::|:|||||:||:
Db        289 AATTATGGCCCTGCT 303


RESULT 15
ABT03391
ID   ABT03391 standard; DNA; 628 BP.
XX
AC   ABT03391;
XX
DT   28-NOV-2002  (first entry)
XX
DE   Ovary cell-specific DNA sequence 107.
XX
KW   Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
KW   ovary specific protein; ovarian cancer; breast cancer; ss; vaccine;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200238606-A2.
XX
PD   16-MAY-2002.
XX
PF   07-NOV-2001; 2001WO-US046459.
XX
PR   08-NOV-2000; 2000US-0246640P.
XX
```

PA (DIAD-) DIADEXUS INC.
XX
PI Sun Y, Recipon H, Salceda S, Liu C;
XX
DR WPI; 2002-519297/55.
XX
PT Polypeptide and polynucleotides present in normal and neoplastic ovary
PT cells, useful for identifying, monitoring, staging, diagnosing,
PT preventing and treating ovarian cancer, and non-cancerous disease states
PT in the ovary.
XX
PS Claim 1; Page 192-193; 247pp; English.
XX
CC The invention comprises amino acid and DNA sequences which are present in
CC normal and neoplastic ovary cells. The DNA and protein sequences of the
CC invention are useful for determining the presence of an ovary specific
CC nucleic acid or an ovary specific protein in a sample. The DNA and
CC protein sequences of the invention are useful for diagnosing and
CC monitoring the presence and metastasis of ovarian cancer and breast
CC cancer. Nucleotides ABT03285 - ABT03421 represents the ovary cell
CC specific DNA sequences of the invention
XX
SQ Sequence 628 BP; 202 A; 115 C; 102 G; 209 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 6; Length 628;
Best Local Similarity 66.7%; Pred. No. 64;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 AAUUAUGGCCCUGCU 17
              ||::|:|||||:||:
Db        305 AATTATGGCCCTGCT 319
```

Search completed: November 29, 2005, 23:12:28
Job time : 223.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 18:29:48 ; Search time 1867.5 Seconds
(without alignments)
450.960 Million cell updates/sec

Title: US-10-018-716B-1
Perfect score: 18
Sequence: 1 gagcagggccataattat 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	17	94.4	794	1	AJ641058	AJ641058 AJ641058
2	16	88.9	312	2	BE153987	BE153987 PM0-HT033
3	16	88.9	340	3	BI432519	BI432519 EST535280
4	16	88.9	439	8	T14826	T14826 crs268 lamb
c 5	16	88.9	500	3	BP191026	BP191026 BP191026
6	16	88.9	652	2	BG600462	BG600462 EST505357
7	16	88.9	740	8	CX409188	CX409188 JGI_XZT32
c 8	16	88.9	747	10	CL169941	CL169941 104_370_1
9	16	88.9	752	10	CW385975	CW385975 fsbb001f0
10	16	88.9	759	2	BG889203	BG889203 EST515054
11	16	88.9	761	10	CL169940	CL169940 104_370_1
c 12	16	88.9	1030	10	CL033121	CL033121 CH216-36A
c 13	15	83.3	85	6	CD963839	CD963839 SDY_133 G
14	15	83.3	95	10	CG560188	CG560188 OST180267
15	15	83.3	102	10	CG671007	CG671007 OST472166
c 16	15	83.3	208	7	CO323095	CO323095 EK189652.
17	15	83.3	238	10	CG556891	CG556891 OST172871
18	15	83.3	247	8	CX626914	CX626914 GAN008N05
19	15	83.3	285	3	BI491822	BI491822 df15e12.w
c 20	15	83.3	306	2	BF353376	BF353376 QV1-HT063
c 21	15	83.3	308	2	BG184004	BG184004 RST2919 A
c 22	15	83.3	336	2	BG790049	BG790049 sae62d11.
c 23	15	83.3	345	3	BM443576	BM443576 EBro02_SQ
c 24	15	83.3	346	2	BB710886	BB710886 BB710886
25	15	83.3	348	5	BU019684	BU019684 QHE22N11.
c 26	15	83.3	365	7	CO190893	CO190893 EK050016.
c 27	15	83.3	374	1	AW020862	AW020862 df15e12.y
28	15	83.3	401	10	AB082236	AB082236 Drosophil
29	15	83.3	405	9	BH388002	BH388002 AG-ND-151
c 30	15	83.3	435	2	BG181938	BG181938 RST797 At
c 31	15	83.3	437	1	AW317773	AW317773 sg57b02.y
c 32	15	83.3	441	2	BG187151	BG187151 RST6134 A
33	15	83.3	444	5	BQ977181	BQ977181 QHI24C10.
c 34	15	83.3	445	6	CA938690	CA938690 sav36e03.
c 35	15	83.3	446	5	BU761255	BU761255 sas65d07.
c 36	15	83.3	449	9	AQ631994	AQ631994 RPCI-11-4
c 37	15	83.3	452	2	BG205213	BG205213 RST24640
38	15	83.3	465	2	BI071352	BI071352 C056P39U
39	15	83.3	471	2	BG187152	BG187152 RST6135 A
c 40	15	83.3	476	1	AW099240	AW099240 sd37a01.y
41	15	83.3	496	8	DN650903	DN650903 G7045.80
c 42	15	83.3	501	2	BG214697	BG214697 RST34346
43	15	83.3	511	1	AI150588	AI150588 qf36g07.x
44	15	83.3	516	1	AL900125	AL900125 AL900125
45	15	83.3	533	8	DN650904	DN650904 G7072.54

ALIGNMENTS

RESULT 1
AJ641058/c
LOCUS AJ641058 794 bp mRNA linear EST 28-JAN-2005
DEFINITION AJ641058 Populus tremula x P. tremuloides/Amanita muscaria mixed EST library Populus tremula x P. tremuloides/Amanita muscaria mixed EST library cDNA clone ptamabc210068e03, mRNA sequence.
ACCESSION AJ641058
VERSION AJ641058.1 GI:58309785
KEYWORDS EST.
SOURCE Populus tremula x P. tremuloides/Amanita muscaria mixed EST library
ORGANISM Populus tremula x P. tremuloides/Amanita muscaria mixed EST library
Eukaryota; mixed EST libraries.
REFERENCE 1 (bases 1 to 794)
AUTHORS Bekel,T., Meyer,F., Kuester,H., Manthey,K., Perlick,A., Puehler,A., Bock,A. and Nehls,U.
TITLE ESTs of fully developed ectomycorrhizas formed between Populus tremula x tremuloides and Amanita muscaria
JOURNAL Unpublished (2005)
COMMENT Contact: Bekel T.
Physiologische Oekologie der Pflanzen
Eberhard-Karls-Universitaet
Auf der Morgenstelle 1, Tuebingen, BW 72076, Germany.
FEATURES Location/Qualifiers
source 1. .794
/organism="Populus tremula x P. tremuloides/Amanita muscaria mixed EST library"
/mol_type="mRNA"
/db_xref="taxon:143775"
/clone="ptamabc210068e03"
/clone_lib="Populus tremula x P. tremuloides/Amanita muscaria mixed EST library"
ORIGIN

Query Match 94.4%; Score 17; DB 1; Length 794;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCAGGGCCATAATTAT 18
||||||||||||||||||
Db 469 AGCAGGGCCATAATTAT 453

RESULT 2
BE153987
LOCUS BE153987 312 bp mRNA linear EST 21-JUN-2000

```
DEFINITION  PM0-HT0339-060400-009-C04 HT0339 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE153987
VERSION     BE153987.1  GI:8616617
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 312)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=PM0-HT0339-060
            400-009-C04&t3=2000-04-06&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 7
            High quality sequence stop: 226.
FEATURES             Location/Qualifiers
     source          1. .312
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HT0339"
                     /note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

  Query Match            88.9%;  Score 16;  DB 2;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCAGGGCCATAATTAT 18
              ||||||||||||||||
Db        274 GCAGGGCCATAATTAT 289


RESULT 3
BI432519
LOCUS       BI432519                340 bp    mRNA    linear   EST 30-APR-2003
DEFINITION  EST535280 P. infestans-challenged potato leaf, compatible reaction
            Solanum tuberosum cDNA clone PPCAR82 5' sequence, mRNA sequence.
ACCESSION   BI432519
VERSION     BI432519.1  GI:15257209
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,
            Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B.
  TITLE     Generation of ESTs from Potato Leaves Challenged with Phytophthora
            infestans, Compatible Interaction
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/
            Seq primer: M13F-R.
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="PPCAR82"
                     /tissue_type="leaf"
                     /dev_stage="6 week old"
                     /lab_host="SOLR"
                     /clone_lib="P. infestans-challenged potato leaf,
                     compatible reaction"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; supplier: Cornell University, Fry lab; sequencing:
                     The Institute for Genomic Research; Whole plants were
                     challenged with 20,000 sporangia/ml of the compatible P.
                     infestans isolate US 940480.  Leaf tissue was collected at
                     3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen
                     in liquid nitrogen immediately upon removal.  Kennebec
                     plants showed first symptoms of infection at 48 hours
                     after inoculation.  NOTE: We cannot exclude the
                     possibility that this sequence is actually derived from
                     Phytophthora rather than potato."
ORIGIN

  Query Match            88.9%;  Score 16;  DB 3;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATT 16
              ||||||||||||||||
Db        268 GAGCAGGGCCATAATT 283


RESULT 4
T14826
LOCUS       T14826                  439 bp    mRNA    linear   EST 28-JUL-1995
DEFINITION  crs268 lambdaZAPST Ricinus communis cDNA clone pcrs268, mRNA
            sequence.
ACCESSION   T14826
VERSION     T14826.1  GI:688463
KEYWORDS    EST.
SOURCE      Ricinus communis (castor bean)
  ORGANISM  Ricinus communis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae;
            Acalypheae; Ricinus.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   vandeLoo,F.J., Turner,S. and Somerville,C.
  TITLE     Expressed sequence tags from developing castor seeds
  JOURNAL   Plant Physiol. 108, 1141-1150 (1995)
COMMENT     Contact: Somerville CR
            Carnegie Institution
            Carnegie Institution, 290 Panama St, Stanford, CA 94305
            Tel: 4153251521
            Email: crs@andrew.stanford.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
```

```
     source          1. .439
                     /organism="Ricinus communis"
                     /mol_type="mRNA"
                     /strain="Baker 296"
                     /db_xref="taxon:3988"
                     /clone="pcrs268"
                     /clone_lib="lambdaZAPST"
                     /note="Vector: lambdaZAPII; Site_1: EcoR1; Site_2: XhoI;
                     Poly(A)+ RNA was purified from developing stage III to
                     stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
                     1982) endosperm plus embryo of immature castor fruits.
                     cDNA was synthesized and cloned into lambdaZAPII according
                     to the instructions of the manufacturer (Stratagene):
                     synthesis was primed from the poly(A) tail, and cloned
                     directionally into XhoI (3') and EcoRI (5') sites.  In few
                     cases, sequence data indicated that this directionality
                     was reversed.  Partial cDNA clones predominate. "
ORIGIN

  Query Match           88.9%;  Score 16;  DB 8;  Length 439;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATT 16
              ||||||||||||||||
Db        317 GAGCAGGGCCATAATT 332


RESULT 5
BP191026/c
LOCUS       BP191026                500 bp    mRNA    linear   EST 17-JUL-2003
DEFINITION  BP191026 planarian head cDNA Dugesia japonica cDNA clone 06171_HH,
            mRNA sequence.
ACCESSION   BP191026
VERSION     BP191026.1  GI:32905550
KEYWORDS    EST.
SOURCE      Dugesia japonica
  ORGANISM  Dugesia japonica
            Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata;
            Tricladida; Paludicola; Dugesiidae; Dugesia.
REFERENCE   1  (bases 1 to 500)
  AUTHORS   Mineta,K., Nakazawa,M., Cebria,F., Ikeo,K., Agata,K. and
            Gojobori,T.
  TITLE     Origin and evolutionary process of the CNS elucidated by
            comparative genomics analysis of planarian ESTs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7666-7671 (2003)
   PUBMED   12802012
COMMENT     Contact: Katsuhiko Mineta
            National Institute of Genetics, Center for Information Biology and
            DNA Data Bank of Japan
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6847
            Fax: 81-559-81-6848
            Email: kmineta@lab.nig.ac.jp
            These clones and additional information are obtained from our web
            site: http://www.cib.nig.ac.jp/dda/.
FEATURES             Location/Qualifiers
     source          1. .500
                     /organism="Dugesia japonica"
                     /mol_type="mRNA"
                     /db_xref="taxon:6161"
                     /clone="06171_HH"
                     /tissue_type="head"
                     /dev_stage="adult"
                     /clone_lib="planarian head cDNA"
ORIGIN

  Query Match           88.9%;  Score 16;  DB 3;  Length 500;
  Best Local Similarity   100.0%;  Pred. No. 1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATTA 17
              ||||||||||||||||
Db        368 AGCAGGGCCATAATTA 353


RESULT 6
BG600462
LOCUS       BG600462                652 bp    mRNA    linear   EST 07-MAR-2003
DEFINITION  EST505357 cSTS Solanum tuberosum cDNA clone cSTS29I1 5' sequence,
            mRNA sequence.
ACCESSION   BG600462
VERSION     BG600462.1  GI:13617598
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 652)
  AUTHORS   van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
            Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
  TITLE     Generations of ESTs from sprouting potato eyes
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/
            Seq primer: M13F-R.
FEATURES             Location/Qualifiers
     source          1. .652
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="cSTS29I1"
                     /tissue_type="sprouting eyes from tubers"
                     /dev_stage="12-14 weeks post harvest"
                     /lab_host="SOLR"
                     /clone_lib="cSTS"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
                     taken from tubers. The tubers were incubated at 26C in the
                     dark for 2-3 weeks prior to sprouting. The eyes were
                     frozen in liquid nitrogen immediately upon removal from
                     tubers."
ORIGIN

  Query Match           88.9%;  Score 16;  DB 2;  Length 652;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATT 16
              ||||||||||||||||
Db        521 GAGCAGGGCCATAATT 536


RESULT 7
CX409188
LOCUS       CX409188                740 bp    mRNA    linear   EST 06-JAN-2005
DEFINITION  JGI_XZT32096.fwd NIH_XGC_tropTad5 Xenopus tropicalis cDNA clone
            IMAGE:7608418 5', mRNA sequence.
ACCESSION   CX409188
VERSION     CX409188.1  GI:57189890
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 740)
  AUTHORS   Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
            Brokstein,P. and Lindquist,E.A.
```

```
  TITLE     DOE Joint Genome Institute Xenopus tropicalis EST project
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Lindquist,E.A., Richardson,P.
            DOE Joint Genome Institute
            2800 Mitchell Drive, Walnut Creek, CA 94598, USA
            Tel: 925 296 5600
            Fax: 925 296 5710
            Email: cdna@jgi-psf.org
            Tissue Procurement: Richard M. Harland Laboratory, University of
            California, Berkeley: http://tropicalis.berkeley.edu/home
            cDNA Library Preparation: Richard M. Harland Laboratory, University
            of California, Berkeley
            DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
            Clone Distribution: I.M.A.G.E. Consortium/LLNL:
            http://image.llnl.gov
            Naming Conventions: EST name is generated by the concatenation of
            the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
            indicates a forward sequencing read of the insert. It does not
            necessarily reflect the orientation of the insert.
            Plate: XZT 0333  row: o  column: 8
            High quality sequence stop: 706.
FEATURES             Location/Qualifiers
     source          1. .740
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="IMAGE:7608418"
                     /tissue_type="whole embryo"
                     /dev_stage="Tadpole (st. 36-41)"
                     /lab_host="E. coli XL1-Blue derivative, Stratagene
                     ElectroTen-Blue"
                     /clone_lib="NIH_XGC_tropTad5"
                     /note="Vector: pCS108; Site_1: SalI; Site_2: NotI; Tadpole
                     library constructed by Russell B. Fletcher in R. Harland's
                     lab using poly A RNA and oligo dT primers (Invitrogen
                     SuperScript Plasmid System for cDNA Synthesis and
                     Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
                     into vector pCS108
                     (http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)
                     ."
ORIGIN

  Query Match            88.9%;  Score 16;  DB 8;  Length 740;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCAGGGCCATAATTAT 18
              ||||||||||||||||
Db         28 GCAGGGCCATAATTAT 43


RESULT 8
CL169941/c
LOCUS       CL169941                747 bp    DNA     linear   GSS 06-JAN-2004
DEFINITION  104_370_10813405_148_31788_109 Sorghum methylation-filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10813405, genomic survey
            sequence.
ACCESSION   CL169941
VERSION     CL169941.1  GI:40682353
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 747)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 370  row: e  column: 13
            Seq primer: SWfor Forward
            Class: methylation filtered
            High quality sequence stop: 747.
FEATURES             Location/Qualifiers
     source          1. .747
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10813405"
                     /clone_lib="Sorghum methylation-filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation-filtered library."
ORIGIN

  Query Match            88.9%;  Score 16;  DB 10;  Length 747;
  Best Local Similarity  100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATTA 17
              ||||||||||||||||
Db        402 AGCAGGGCCATAATTA 387


RESULT 9
CW385975
LOCUS       CW385975                752 bp    DNA     linear   GSS 01-NOV-2004
DEFINITION  fsbb001f069k13k0 Sorghum methylation filtered library (LibID: 104)
            Sorghum bicolor genomic clone fsbb001f069k13, genomic survey
            sequence.
ACCESSION   CW385975
VERSION     CW385975.1  GI:55104419
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 752)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: fsbb001f069  row: k  column: 13
            Seq primer: k Reverse
            Class: methylation filtered
            High quality sequence stop: 752.
FEATURES             Location/Qualifiers
     source          1. .752
                     /organism="Sorghum bicolor"
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                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="fsbb001f069k13"
                     /clone_lib="Sorghum methylation filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation filtered library."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 10;  Length 752;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATTA 17
              ||||||||||||||||
Db        599 AGCAGGGCCATAATTA 614


RESULT 10
BG889203
LOCUS       BG889203                759 bp    mRNA    linear   EST 07-MAR-2003
DEFINITION  EST515054 cSTD Solanum tuberosum cDNA clone cSTD13G2 5' sequence,
            mRNA sequence.
ACCESSION   BG889203
VERSION     BG889203.1  GI:14266289
KEYWORDS    EST.
SOURCE      Solanum tuberosum (potato)
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 759)
  AUTHORS   van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemingo,A.,
            Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
  TITLE     Generations of ESTs from dormant potato tubers
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            This clone can be obtained from the University of Arizona Genomics
            Institute. Orders can be made through URL:
            http://genome.arizona.edu/orders/
            Seq primer: M13F-R.
FEATURES             Location/Qualifiers
     source          1. .759
                     /organism="Solanum tuberosum"
                     /mol_type="mRNA"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="cSTD13G2"
                     /tissue_type="dormant tuber"
                     /dev_stage="one month post-harvest"
                     /lab_host="SOLR"
                     /clone_lib="cSTD"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; This library targets genes expressed in dormant
                     tubers. This library was made from sections of dormant
                     tuber, avoiding the buds and epidermis. Tubers were stored
                     for one month post-harvest at 4oC. The tuber was peeled,
                     well away from the surface. Then it was chopped into 1-2
                     mm cubes and immediately frozen in liquid nitrogen. This
                     library is noted as P4 in Tanksley lab notebooks."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 2;  Length 759;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATT 16
              ||||||||||||||||
Db        606 GAGCAGGGCCATAATT 621


RESULT 11
CL169940
LOCUS       CL169940                761 bp    DNA     linear   GSS 06-JAN-2004
DEFINITION  104_370_10813405_116_31789_109 Sorghum methylation-filtered library
            (LibID: 104) Sorghum bicolor genomic clone 10813405, genomic survey
            sequence.
ACCESSION   CL169940
VERSION     CL169940.1  GI:40682352
KEYWORDS    GSS.
SOURCE      Sorghum bicolor (sorghum)
  ORGANISM  Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1  (bases 1 to 761)
  AUTHORS   Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,
            Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,
            McMenamy,J., Smith,M., Holeman,H., Roe,B.A, Wiley,G., Korf,I.F.,
            Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and
            Martienssen,R.A.
  TITLE     Sorghum genome sequencing by methylation filtration
  JOURNAL   PLoS Biol. 3 (1), e13 (2005)
   PUBMED   15660154
COMMENT     Contact: Bedell JA
            Orion Genomics, LLC
            4041 Forest Park Ave, St. Louis, MO 63108, USA
            Tel: 314 615 6979
            Fax: 314 615 5975
            Email: jbedell@oriongenomics.com
            Plate: 370  row: e  column: 13
            Seq primer: T3 Reverse
            Class: methylation filtered
            High quality sequence stop: 761.
FEATURES             Location/Qualifiers
     source          1. .761
                     /organism="Sorghum bicolor"
                     /mol_type="genomic DNA"
                     /cultivar="ATx623"
                     /db_xref="taxon:4558"
                     /clone="10813405"
                     /clone_lib="Sorghum methylation-filtered library (LibID:
                     104)"
                     /note="Organ: leaf; Vector: pBCSK(-); Site_1: HincII; DNA
                     prepared from purified nuclei was randomly sheared,
                     end-repaired, size fractionated to enrich for the 0.5 to 5
                     kb fraction, ligated into HincII-digested pBCSK(-) vector
                     and electroporated into E. coli cells. This is a
                     methylation-filtered library."
ORIGIN

  Query Match             88.9%;  Score 16;  DB 10;  Length 761;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATTA 17
              ||||||||||||||||
Db        639 AGCAGGGCCATAATTA 654


RESULT 12
CL033121/c
LOCUS       CL033121                1030 bp    DNA     linear   GSS 31-DEC-2003
DEFINITION  CH216-36A12_Sp6.1 CH216 Xenopus tropicalis genomic clone
            CH216-36A12, genomic survey sequence.
ACCESSION   CL033121
VERSION     CL033121.1  GI:40483484
KEYWORDS    GSS.
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SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 1030)
  AUTHORS   Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
            Mardis,E. and Wilson,R.
  TITLE     A physical map of the xenopus tropicalis genome
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Insert Length: 175000   Std Error: 0.00
            Seq primer: Sp6 ATTTAGGTGACACTATAG
            Class: BAC ends
            High quality sequence start: 29
            High quality sequence stop: 943.
FEATURES             Location/Qualifiers
     source          1. .1030
                     /organism="Xenopus tropicalis"
                     /mol_type="genomic DNA"
                     /strain="Nigerian frog"
                     /db_xref="taxon:8364"
                     /clone="CH216-36A12"
                     /sex="male"
                     /cell_line="Stock 248 F7A2, inbred N7"
                     /clone_lib="CH216"
                     /note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                     BAC library"
ORIGIN

  Query Match             88.9%;  Score 16;  DB 10;  Length 1030;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCAGGGCCATAATTAT 18
              ||||||||||||||||
Db         47 GCAGGGCCATAATTAT 32


RESULT 13
CD963839/c
LOCUS       CD963839                 85 bp    mRNA    linear   EST 16-JUL-2003
DEFINITION  SDY_133 GeneTag2 Zea mays cDNA, mRNA sequence.
ACCESSION   CD963839
VERSION     CD963839.1  GI:32824117
KEYWORDS    EST.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 85)
  AUTHORS   Genoplante.
  TITLE     Genoplante, a major partnership french program in plant genomics
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Genoplante
            Genoplante
            93, rue Henri Rochefort 91025 EVRY CEDEX France
            Tel: 33 1 69 47 54 00
            Fax: 33 1 69 47 54 10
            This sequence has been generated in the framework of the french
            plant genomics programme 'Genoplante' (http://www.genoplante.com
            and http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .85
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /cultivar="mixture"
                     /db_xref="taxon:4577"
                     /clone_lib="GeneTag2"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAAT 15
              |||||||||||||||
Db         61 GAGCAGGGCCATAAT 47


RESULT 14
CG560188
LOCUS       CG560188                 95 bp    mRNA    linear   GSS 01-OCT-2003
DEFINITION  OST180267 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST180267,
            mRNA sequence.
ACCESSION   CG560188
VERSION     CG560188.1  GI:37346775
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 95)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
   PUBMED   14610273
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .95
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                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST180267"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             83.3%;  Score 15;  DB 10;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCAGGGCCATAATTA 17
              |||||||||||||||
Db         37 GCAGGGCCATAATTA 51


RESULT 15
CG671007
LOCUS       CG671007                102 bp    mRNA    linear   GSS 02-OCT-2003
DEFINITION  OST472166 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST472166,
            mRNA sequence.
ACCESSION   CG671007
VERSION     CG671007.1  GI:37494856
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 102)
  AUTHORS   Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
            Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
            Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
            Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
            Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
            Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
            Zhu,Q., Person,C. and Sands,A.T.
  TITLE     Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
            screen to identify potential targets for therapeutic intervention
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
   PUBMED   14610273
COMMENT     Contact: Zambrowicz BP
            OmniBank
            Lexicon Genetics Incorporated
            4000 Research Forest Drive, The Woodlands, TX 77381, USA
            Email: materials@lexgen.com
            Gene trap sequence tag generated by 3' RACE from mouse ES cells as
            described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .102
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="129Sv/Ev"
                     /db_xref="taxon:10090"
                     /clone="OST472166"
                     /cell_type="embryonic stem cell"
                     /clone_lib="Mus musculus 129Sv/Ev"
ORIGIN

  Query Match             83.3%;  Score 15;  DB 10;  Length 102;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCAGGGCCATAATTA 17
              |||||||||||||||
Db         28 GCAGGGCCATAATTA 42


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Job time : 1871.5 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 17:06:31 ; Search time 136.5 Seconds
(without alignments)
19.597 Million cell updates/sec

Title: US-10-018-716B-1
Perfect score: 18
Sequence: 1 gagcagggccataattat 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3205263 seqs, 74304013 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6410526

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	14	77.8	1149	9	US-11-082-389-213	Sequence 213, App
c	2	12	66.7	19	8	US-11-101-244-173294	Sequence 173294,
	3	12	66.7	19	8	US-11-101-244-339765	Sequence 339765,
c	4	12	66.7	19	8	US-11-101-244-600029	Sequence 600029,
c	5	12	66.7	19	8	US-11-101-244-1044082	Sequence 1044082,
c	6	12	66.7	19	8	US-11-101-244-1044118	Sequence 1044118,
c	7	12	66.7	19	8	US-11-101-244-1152178	Sequence 1152178,
c	8	12	66.7	19	8	US-11-101-244-1152276	Sequence 1152276,
c	9	12	66.7	19	8	US-11-101-244-1311535	Sequence 1311535,
	10	12	66.7	19	8	US-11-101-244-1430673	Sequence 1430673,
	11	12	66.7	19	8	US-11-101-244-1430674	Sequence 1430674,
c	12	12	66.7	19	9	US-11-083-784-173294	Sequence 173294,
	13	12	66.7	19	9	US-11-083-784-339765	Sequence 339765,
c	14	12	66.7	19	9	US-11-083-784-600029	Sequence 600029,
c	15	12	66.7	19	9	US-11-083-784-1044082	Sequence 1044082,
c	16	12	66.7	19	9	US-11-083-784-1044118	Sequence 1044118,
c	17	12	66.7	19	9	US-11-083-784-1152178	Sequence 1152178,
c	18	12	66.7	19	9	US-11-083-784-1152276	Sequence 1152276,
c	19	12	66.7	19	9	US-11-083-784-1311535	Sequence 1311535,
	20	12	66.7	19	9	US-11-083-784-1430673	Sequence 1430673,
	21	12	66.7	19	9	US-11-083-784-1430674	Sequence 1430674,
	22	12	66.7	844	9	US-11-082-389-441	Sequence 441, App
	23	12	66.7	1095	9	US-11-082-389-439	Sequence 439, App
c	24	12	66.7	1656	1	US-10-131-826A-239	Sequence 239, App
	25	12	66.7	3458	1	US-10-793-626-3510	Sequence 3510, Ap
c	26	12	66.7	6708	1	US-10-821-234-164	Sequence 164, App
c	27	12	66.7	7382	1	US-10-839-211-1	Sequence 1, Appli
c	28	11	61.1	19	8	US-11-101-244-341877	Sequence 341877,
	29	11	61.1	19	8	US-11-101-244-343613	Sequence 343613,
	30	11	61.1	19	8	US-11-101-244-343631	Sequence 343631,
	31	11	61.1	19	8	US-11-101-244-374101	Sequence 374101,
	32	11	61.1	19	8	US-11-101-244-380293	Sequence 380293,
	33	11	61.1	19	8	US-11-101-244-425500	Sequence 425500,
	34	11	61.1	19	8	US-11-101-244-425510	Sequence 425510,
	35	11	61.1	19	8	US-11-101-244-425572	Sequence 425572,
	36	11	61.1	19	8	US-11-101-244-661639	Sequence 661639,
	37	11	61.1	19	8	US-11-101-244-661697	Sequence 661697,
c	38	11	61.1	19	8	US-11-101-244-716963	Sequence 716963,
c	39	11	61.1	19	8	US-11-101-244-716974	Sequence 716974,
	40	11	61.1	19	8	US-11-101-244-725866	Sequence 725866,
	41	11	61.1	19	8	US-11-101-244-764763	Sequence 764763,
	42	11	61.1	19	8	US-11-101-244-764784	Sequence 764784,
	43	11	61.1	19	8	US-11-101-244-764830	Sequence 764830,
	44	11	61.1	19	8	US-11-101-244-799257	Sequence 799257,
	45	11	61.1	19	8	US-11-101-244-828288	Sequence 828288,

ALIGNMENTS

RESULT 1
US-11-082-389-213/c
; Sequence 213, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 213
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1126)
; OTHER INFORMATION: RXN00523

US-11-082-389-213

Query Match 77.8%; Score 14; DB 9; Length 1149;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGCAGGGCCATAA 14
              ||||||||||||||
Db        242 GAGCAGGGCCATAA 229
```

RESULT 2
US-11-101-244-173294/c
; Sequence 173294, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 173294
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-173294

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 AGCAGGGCCATA 13
              ||||||||||||
Db         14 AGCAGGGCCATA 3
```

RESULT 3
US-11-101-244-339765
; Sequence 339765, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 339765
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-339765

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 GGGCCATAATTA 17
              ||||||:||::|
Db          8 GGGCCAUAAUUA 19
```

RESULT 4
US-11-101-244-600029/c
; Sequence 600029, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 600029
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-600029

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGCAGGGCCAT 12
              ||||||||||||
Db         14 GAGCAGGGCCAT 3
```

RESULT 5
US-11-101-244-1044082/c
; Sequence 1044082, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1044082
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1044082

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGCAGGGCCAT 12
              ||||||||||||
Db         14 GAGCAGGGCCAT 3
```

RESULT 6
US-11-101-244-1044118/c
; Sequence 1044118, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1044118
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1044118

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGCAGGGCCAT 12
              ||||||||||||
Db         16 GAGCAGGGCCAT 5
```

RESULT 7
US-11-101-244-1152178/c
; Sequence 1152178, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1152178
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1152178

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGCAGGGCCAT 12
              ||||||||||||
Db         16 GAGCAGGGCCAT 5
```

RESULT 8
US-11-101-244-1152276/c
; Sequence 1152276, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1152276
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1152276

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGCAGGGCCAT 12
              ||||||||||||
Db         16 GAGCAGGGCCAT 5
```

RESULT 9
US-11-101-244-1311535/c
; Sequence 1311535, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1311535
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1311535

Query Match 66.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;

```
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GGCCATAATTAT 18
              ||||||||||||
Db         14 GGCCATAATTAT 3


RESULT 10
US-11-101-244-1430673
; Sequence 1430673, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1430673
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1430673

  Query Match             66.7%;  Score 12;  DB 8;  Length 19;
  Best Local Similarity   91.7%;  Pred. No. 34;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCAT 12
              ||||||||||| :
Db          1 GAGCAGGGCCAU 12


RESULT 11
US-11-101-244-1430674
; Sequence 1430674, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1430674
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1430674

  Query Match             66.7%;  Score 12;  DB 8;  Length 19;
  Best Local Similarity   91.7%;  Pred. No. 34;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCAT 12
              ||||||||||| :
Db          4 GAGCAGGGCCAU 15


RESULT 12
US-11-083-784-173294/c
; Sequence 173294, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 173294
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-173294

  Query Match             66.7%;  Score 12;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 34;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATA 13
              ||||||||||||
Db         14 AGCAGGGCCATA 3


RESULT 13
US-11-083-784-339765
; Sequence 339765, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 339765
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-339765
```

Query Match 66.7%; Score 12; DB 9; Length 19;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          6 GGGCCATAATTA 17
              ||||||:||::|
Db          8 GGGCCAUAAUUA 19
```

RESULT 14
US-11-083-784-600029/c
; Sequence 600029, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 600029
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-600029

Query Match 66.7%; Score 12; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGCAGGGCCAT 12
              ||||||||||||
Db         14 GAGCAGGGCCAT 3
```

RESULT 15
US-11-083-784-1044082/c
; Sequence 1044082, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1044082
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1044082

Query Match 66.7%; Score 12; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAGCAGGGCCAT 12
              ||||||||||||
Db         14 GAGCAGGGCCAT 3
```

Search completed: November 29, 2005, 18:29:39
Job time : 137.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 17:06:35 ; Search time 403.5 Seconds
(without alignments)
368.894 Million cell updates/sec

Title: US-10-018-716B-1
Perfect score: 18
Sequence: 1 gagcagggccataattat 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	18	100.0	441	4	US-09-925-065A-192589	Sequence 192589,
c	2	18	100.0	441	4	US-09-925-065A-192590	Sequence 192590,
c	3	18	100.0	1922	8	US-10-349-528-4	Sequence 4, Appli
c	4	18	100.0	2019	7	US-10-382-248-9	Sequence 9, Appli
c	5	18	100.0	2393	5	US-10-225-567A-121	Sequence 121, App
c	6	18	100.0	2393	5	US-10-207-655-64	Sequence 64, Appl
c	7	18	100.0	2393	6	US-10-305-720-1209	Sequence 1209, Ap
c	8	16	88.9	201	8	US-10-719-993-38475	Sequence 38475, A
c	9	16	88.9	612	4	US-09-925-065A-391076	Sequence 391076,
c	10	16	88.9	261638	8	US-10-719-993-6882	Sequence 6882, Ap
c	11	15	83.3	461	4	US-09-925-065A-328046	Sequence 328046,
	12	15	83.3	507	6	US-10-172-118-2085	Sequence 2085, Ap
	13	15	83.3	507	7	US-10-342-887-2085	Sequence 2085, Ap
	14	15	83.3	533	4	US-09-925-065A-520324	Sequence 520324,
	15	15	83.3	544	4	US-09-925-065A-539398	Sequence 539398,
c	16	15	83.3	612	5	US-10-007-280A-106	Sequence 106, App
c	17	15	83.3	628	5	US-10-007-280A-107	Sequence 107, App
	18	15	83.3	842	5	US-10-027-632-160723	Sequence 160723,
	19	15	83.3	842	5	US-10-027-632-160724	Sequence 160724,
	20	15	83.3	842	6	US-10-027-632-160723	Sequence 160723,
	21	15	83.3	842	6	US-10-027-632-160724	Sequence 160724,
c	22	15	83.3	1634	7	US-10-424-599-84619	Sequence 84619, A
	23	15	83.3	2021	8	US-10-739-930-4619	Sequence 4619, Ap
c	24	15	83.3	3659	10	US-11-097-143-15251	Sequence 15251, A
c	25	15	83.3	9140	10	US-11-097-143-15250	Sequence 15250, A
	26	15	83.3	76829	9	US-10-737-082-27	Sequence 27, Appl
	27	15	83.3	76829	9	US-10-765-790-27	Sequence 27, Appl
c	28	15	83.3	180227	7	US-10-322-281-308	Sequence 308, App
c	29	15	83.3	202251	5	US-10-087-192-985	Sequence 985, App
	30	15	83.3	325348	6	US-10-085-117-358	Sequence 358, App
c	31	14	77.8	25	8	US-10-719-900-825663	Sequence 825663,
	32	14	77.8	219	7	US-10-437-963-7570	Sequence 7570, Ap
c	33	14	77.8	285	8	US-10-425-115-95091	Sequence 95091, A
c	34	14	77.8	465	4	US-09-925-065A-622260	Sequence 622260,
c	35	14	77.8	465	4	US-09-925-065A-622261	Sequence 622261,
c	36	14	77.8	465	4	US-09-925-065A-622262	Sequence 622262,
	37	14	77.8	574	5	US-10-066-543-3296	Sequence 3296, Ap
c	38	14	77.8	591	5	US-10-027-632-15415	Sequence 15415, A
c	39	14	77.8	591	5	US-10-027-632-15416	Sequence 15416, A
c	40	14	77.8	591	6	US-10-027-632-15415	Sequence 15415, A
c	41	14	77.8	591	6	US-10-027-632-15416	Sequence 15416, A
	42	14	77.8	600	4	US-09-925-065A-895996	Sequence 895996,
	43	14	77.8	611	5	US-10-027-632-224562	Sequence 224562,
	44	14	77.8	611	6	US-10-027-632-224562	Sequence 224562,
c	45	14	77.8	668	7	US-10-437-963-3301	Sequence 3301, Ap

ALIGNMENTS

RESULT 1
US-09-925-065A-192589/c
; Sequence 192589, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 192589
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-192589

Query Match 100.0%; Score 18; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db        335 GAGCAGGGCCATAATTAT 318
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RESULT 2
US-09-925-065A-192590/c
; Sequence 192590, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

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;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 192590
;   LENGTH: 441
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-192590

  Query Match            100.0%;  Score 18;  DB 4;  Length 441;
  Best Local Similarity   100.0%;  Pred. No. 0.47;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db        335 GAGCAGGGCCATAATTAT 318


RESULT 3
US-10-349-528-4/c
; Sequence 4, Application US/10349528
; Publication No. US20040253668A1
; GENERAL INFORMATION:
;  APPLICANT: RAMANATHAN, Chandra
;  APPLICANT:  GOPAL, Shuba
;  APPLICANT:  MINTIER, Gabe
;  APPLICANT:  FEDER, John
;  TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
;  TITLE OF INVENTION:  USE THEREOF
;  FILE REFERENCE: D0210
;  CURRENT APPLICATION NUMBER: US/10/349,528
;  CURRENT FILING DATE:  2003-01-22
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 1922
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-10-349-528-4

  Query Match            100.0%;  Score 18;  DB 8;  Length 1922;
  Best Local Similarity   100.0%;  Pred. No. 0.48;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         28 GAGCAGGGCCATAATTAT 11


RESULT 4
US-10-382-248-9/c
; Sequence 9, Application US/10382248
; Publication No. US20040058347A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, et al.
;  TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-568C
;  CURRENT APPLICATION NUMBER: US/10/382,248
;  CURRENT FILING DATE:  2003-03-05
;  PRIOR APPLICATION NUMBER: 60/366,928
;  PRIOR FILING DATE: 2002-03-22
;  PRIOR APPLICATION NUMBER: 60/361,974
;  PRIOR FILING DATE: 2002-03-06
;  PRIOR APPLICATION NUMBER: 60/365,477
;  PRIOR FILING DATE: 2002-03-19
;  PRIOR APPLICATION NUMBER: 60/401,661
;  PRIOR FILING DATE: 2002-08-06
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 9
;   LENGTH: 2019
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (61)..(1959)
US-10-382-248-9

  Query Match            100.0%;  Score 18;  DB 7;  Length 2019;
  Best Local Similarity   100.0%;  Pred. No. 0.48;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         72 GAGCAGGGCCATAATTAT 55


RESULT 5
US-10-225-567A-121/c
; Sequence 121, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 121
;   LENGTH: 2393
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-225-567A-121

  Query Match            100.0%;  Score 18;  DB 5;  Length 2393;
  Best Local Similarity   100.0%;  Pred. No. 0.48;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         78 GAGCAGGGCCATAATTAT 61


RESULT 6
US-10-207-655-64/c
; Sequence 64, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
;  APPLICANT: Ledbetter, Jeffrey A.
;  APPLICANT:  Hayden-Ledbetter, Martha S.
;  TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
;  FILE REFERENCE: 390069.401C1
;  CURRENT APPLICATION NUMBER: US/10/207,655
;  CURRENT FILING DATE:  2002-07-25
;  NUMBER OF SEQ ID NOS: 426
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 64
;   LENGTH: 2393
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-207-655-64

  Query Match             100.0%;  Score 18;  DB 5;  Length 2393;
  Best Local Similarity   100.0%;  Pred. No. 0.48;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         78 GAGCAGGGCCATAATTAT 61


RESULT 7
US-10-305-720-1209/c
; Sequence 1209, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
;  APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
;  TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
;  FILE REFERENCE: PA-0002-1 CON
;  CURRENT APPLICATION NUMBER: US/10/305,720
;  CURRENT FILING DATE:  2002-11-26
;  PRIOR APPLICATION NUMBER: 09/016,434
;  PRIOR FILING DATE: 1998-01-30
;  NUMBER OF SEQ ID NOS: 1490
;  SOFTWARE: PERL Program
; SEQ ID NO 1209
;   LENGTH: 2393
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GenBank ID No. US20040010136A1 g182770
US-10-305-720-1209

  Query Match             100.0%;  Score 18;  DB 6;  Length 2393;
  Best Local Similarity   100.0%;  Pred. No. 0.48;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         78 GAGCAGGGCCATAATTAT 61


RESULT 8
US-10-719-993-38475/c
; Sequence 38475, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001496
;  CURRENT APPLICATION NUMBER: US/10/719,993
;  CURRENT FILING DATE:  2003-11-24
;  NUMBER OF SEQ ID NOS: 55342
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38475
;   LENGTH: 201
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-719-993-38475

  Query Match             88.9%;  Score 16;  DB 8;  Length 201;
  Best Local Similarity   100.0%;  Pred. No. 7.7;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCAGGGCCATAATTAT 18
              ||||||||||||||||
Db        128 GCAGGGCCATAATTAT 113


RESULT 9
US-09-925-065A-391076/c
; Sequence 391076, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 391076
;   LENGTH: 612
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-391076

  Query Match             88.9%;  Score 16;  DB 4;  Length 612;
  Best Local Similarity   100.0%;  Pred. No. 7.8;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATTA 17
              ||||||||||||||||
Db        580 AGCAGGGCCATAATTA 565


RESULT 10
US-10-719-993-6882/c
; Sequence 6882, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001496
;  CURRENT APPLICATION NUMBER: US/10/719,993
;  CURRENT FILING DATE:  2003-11-24
;  NUMBER OF SEQ ID NOS: 55342
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6882
;   LENGTH: 261638
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-719-993-6882

  Query Match             88.9%;  Score 16;  DB 8;  Length 261638;
  Best Local Similarity   100.0%;  Pred. No. 8.4;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GCAGGGCCATAATTAT 18
              ||||||||||||||||
Db      29154 GCAGGGCCATAATTAT 29139


RESULT 11
US-09-925-065A-328046/c
; Sequence 328046, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
```

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;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 328046
;   LENGTH: 461
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-328046

  Query Match             83.3%;  Score 15;  DB 4;  Length 461;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATT 16
              ||||||||||||||||
Db         25 AGCAGGGCCATAATT 11


RESULT 12
US-10-172-118-2085
; Sequence 2085, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
;  APPLICANT: Dai, Hongyue
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Chris
;  APPLICANT:  Van 't Veer, Laura
;  APPLICANT:  Van de Vijver, Marc
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-175-999
;  CURRENT APPLICATION NUMBER: US/10/172,118
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: 60/380,770
;  PRIOR FILING DATE: 2002-05-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2085
;   LENGTH: 507
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: Contig23454
;   DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-2085

  Query Match             83.3%;  Score 15;  DB 6;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATT 16
              ||||||||||||||||
Db        163 AGCAGGGCCATAATT 177


RESULT 13
US-10-342-887-2085
; Sequence 2085, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
;  APPLICANT: Dai, Hongyue
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter S.
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Christopher J.
;  APPLICANT:  Van 't Veer, Laura Johanna
;  APPLICANT:  Van de Vijver, Marc J.
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-188-999
;  CURRENT APPLICATION NUMBER: US/10/342,887
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: 60/298,918
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: 60/380,710
;  PRIOR FILING DATE: 2002-05-14
;  PRIOR APPLICATION NUMBER: 10/172,118
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 2085
;   LENGTH: 507
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-342-887-2085

  Query Match             83.3%;  Score 15;  DB 7;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATT 16
              ||||||||||||||||
Db        163 AGCAGGGCCATAATT 177


RESULT 14
US-09-925-065A-520324
; Sequence 520324, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single
;  TITLE OF INVENTION:  Nucleotide Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.135
;  CURRENT APPLICATION NUMBER: US/09/925,065A
;  CURRENT FILING DATE:  2001-08-08
;  PRIOR APPLICATION NUMBER: US 60/243,096
;  PRIOR FILING DATE: 2000-10-24
;  PRIOR APPLICATION NUMBER: US 60/252,147
;  PRIOR FILING DATE: 2000-11-20
;  PRIOR APPLICATION NUMBER: US 60/250,092
;  PRIOR FILING DATE: 2000-11-30
;  PRIOR APPLICATION NUMBER: US 60/261,766
;  PRIOR FILING DATE: 2001-01-16
;  PRIOR APPLICATION NUMBER: US 60/289,846
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 957086
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 520324
;   LENGTH: 533
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-925-065A-520324

  Query Match             83.3%;  Score 15;  DB 4;  Length 533;
  Best Local Similarity   100.0%;  Pred. No. 32;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATT 16
              ||||||||||||||||
Db        354 AGCAGGGCCATAATT 368
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RESULT 15
US-09-925-065A-539398
; Sequence 539398, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 539398
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-539398

Query Match 83.3%; Score 15; DB 4; Length 544;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 AGCAGGGCCATAATT 16
              |||||||||||||||
Db        354 AGCAGGGCCATAATT 368
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Title: US-10-018-716B-1
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Sequence: 1 gagcagggccataattat 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
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14: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	18	100.0	856	8	HSFSTHR	X68044 H.sapiens m
c 2	18	100.0	1724	8	S73199	S73199 follicle-st
c 3	18	100.0	1734	8	HSFSHX1	Z34260 H.sapiens D
c 4	18	100.0	2179	6	AR003719	AR003719 Sequence
c 5	18	100.0	2179	6	AR067576	AR067576 Sequence
c 6	18	100.0	2179	6	AR207283	AR207283 Sequence
c 7	18	100.0	2179	8	S59900	S59900 follicle st
c 8	18	100.0	2186	8	HUMFSHREC	M95489 H.sapiens f
c 9	18	100.0	2222	6	A76125	A76125 Sequence 1
c 10	18	100.0	2374	6	CQ715054	CQ715054 Sequence
c 11	18	100.0	2393	6	AR270646	AR270646 Sequence
c 12	18	100.0	2393	6	AX548836	AX548836 Sequence
c 13	18	100.0	2393	8	HUMFSHRE	M65085 Human folli
14	18	100.0	121688	8	AC092533	AC092533 Homo sapi
15	18	100.0	158709	14	AC083827	AC083827 Homo sapi
c 16	17	94.4	162	8	HSFSHRX1	X91738 H.sapiens g
c 17	16	88.9	1041	5	AY625217	AY625217 Priotelus
18	16	88.9	95681	8	AL157890	AL157890 Human DNA
c 19	16	88.9	113657	14	AC166226	AC166226 Sorex ara
c 20	16	88.9	121589	14	AC137655	AC137655 Bos tauru
c 21	16	88.9	125311	8	AC068758	AC068758 Homo sapi
c 22	16	88.9	127015	14	AC151504	AC151504 Dasypus n
c 23	16	88.9	160179	14	AC092930	AC092930 Homo sapi
c 24	16	88.9	168380	8	AC063933	AC063933 Homo sapi
c 25	16	88.9	169314	14	AC148413	AC148413 Callithri
c 26	16	88.9	169996	14	AC053521	AC053521 Homo sapi
27	16	88.9	171267	14	AC154087	AC154087 Alligator
c 28	16	88.9	171990	14	AC153783	AC153783 Rhinoloph
c 29	16	88.9	185798	14	AC158248	AC158248 Callithri
c 30	16	88.9	187465	9	AC132305	AC132305 Mus muscu
c 31	16	88.9	191709	9	AC115890	AC115890 Mus muscu
32	16	88.9	197909	9	AC158658	AC158658 Mus muscu
c 33	16	88.9	198551	9	AC068605	AC068605 Mus muscu
c 34	16	88.9	210236	14	AC150699	AC150699 Bos tauru
c 35	16	88.9	236157	14	AC111356	AC111356 Rattus no
c 36	16	88.9	256499	14	AC130987	AC130987 Rattus no
c 37	16	88.9	283919	14	AC095169	AC095169 Rattus no
c 38	15	83.3	481	6	AR496706	AR496706 Sequence
c 39	15	83.3	481	6	AR511988	AR511988 Sequence
c 40	15	83.3	612	6	AX554759	AX554759 Sequence
c 41	15	83.3	628	6	AX554760	AX554760 Sequence
c 42	15	83.3	1303	5	CR760514	CR760514 Xenopus t
c 43	15	83.3	1437	5	BC061373	BC061373 Xenopus t
44	15	83.3	1727	15	AB023467	AB023467 Metschnik
45	15	83.3	2652	8	BC034230	BC034230 Homo sapi

ALIGNMENTS

RESULT 1
HSFSTHR/c
LOCUS HSFSTHR 856 bp mRNA linear PRI 07-FEB-1993
DEFINITION H.sapiens mRNA for follicle-stimulating hormone receptor.
ACCESSION X68044
VERSION X68044:1 GI:31473
KEYWORDS follicle stimulating hormone receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 856)
AUTHORS Gromoll,J., Gudermann,T. and Nieschlag,E.
TITLE Molecular cloning of a truncated isoform of the human follicle stimulating hormone receptor
JOURNAL Biochem. Biophys. Res. Commun. 188 (3), 1077-1083 (1992)
PUBMED 1359889
REFERENCE 2
AUTHORS Gromoll,J.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1992) J. Gromoll, Institut f Reproduktionsmedizin, Steinfurter Strasse 107, 4400 Muenster, FRG
FEATURES Location/Qualifiers
source 1. .856
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="testis"
CDS 17. .856
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ERNSFVGLSFESVILWLNKNGIQEIHNCAFNGTQLDELNLSDNNNLEELPNDVFHGAS
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NEVV"
ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 856;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
||||||||||||||||||
Db 28 GAGCAGGGCCATAATTAT 11

RESULT 2
S73199/c
LOCUS S73199 1724 bp DNA linear PRI 28-FEB-1995
DEFINITION follicle-stimulating hormone receptor (5' region) [human, Genomic, 1724 nt].
ACCESSION S73199
VERSION S73199.1 GI:685036
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1724)
AUTHORS Gromoll,J., Dankbar,B. and Gudermann,T.
TITLE Characterization of the 5' flanking region of the human follicle-stimulating hormone receptor gene
JOURNAL Mol. Cell. Endocrinol. 102 (1-2), 93-102 (1994)
PUBMED 7926278
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 155309] from the original journal article.
FEATURES Location/Qualifiers
source 1. .1724
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene 1487. .1642
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CDS 1487. .1642
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/note="FSHR"
/codon_start=1
/product="follicle-stimulating hormone receptor"
/protein_id="AAB32071.1"
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/translation="MALLLVSLLAFLSLGSGCHHRICHCSNRVFLCQESKVTEIPSDL PRNAIEL"
ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 1724;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
||||||||||||||||||
Db 1498 GAGCAGGGCCATAATTAT 1481

RESULT 3
HSFSHX1/c
LOCUS HSFSHX1 1734 bp DNA linear PRI 24-JUL-1995
DEFINITION H.sapiens DNA for follicle stimulating hormone (FSH) receptor.
ACCESSION Z34260
VERSION Z34260.1 GI:1052701
KEYWORDS follicle stimulating hormone receptor; FSH-receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1734)
AUTHORS Gromoll,J.
JOURNAL Thesis (1994) Institute of Reproductive Medicine, University of Muenster
REFERENCE 2 (bases 1 to 1734)
AUTHORS Gromoll,J.
TITLE Characterization of the 5'-flanking region of the human follicle stimulating hormone receptor gene
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1734)
AUTHORS Gromoll,J.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-1994) Gromoll J., University of Muenster Institute of Reproductive Medicine Steinfurter Str. 107 Muenster Germany 48149
FEATURES Location/Qualifiers
source 1. .1734
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/cell_type="Leukocyte"
/tissue_type="Blood"
/clone_lib="genomic EMBL3"
exon 1487. .1647
/product="FSH receptor"
/number=1
intron 1648. .>1734
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ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 1734;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
||||||||||||||||||
Db 1498 GAGCAGGGCCATAATTAT 1481

RESULT 4
AR003719/c
LOCUS AR003719 2179 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 1 from patent US 5744448.
ACCESSION AR003719
VERSION AR003719.1 GI:3964978
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2179)
AUTHORS Kelton,C.Ann., Cheng,S.Vui.Yen., Nugent,N.Patrice. and Schweickhardt,R.Lynn.
TITLE Human follicle stimulating hormone receptor
JOURNAL Patent: US 5744448-A 1 28-APR-1998;
FEATURES Location/Qualifiers
source 1. .2179
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 2179;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
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Db 86 GAGCAGGGCCATAATTAT 69

RESULT 5
AR067576/c
LOCUS AR067576 2179 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5851768.
ACCESSION AR067576

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VERSION     AR067576.1  GI:5998798
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2179)
  AUTHORS   de la Chapelle,A., Huhtaniemi,I. and Aittomaki,K.
  TITLE     Method for diagnosis of ovarian dysgenesis
  JOURNAL   Patent: US 5851768-A 1 22-DEC-1998;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.6;
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Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         86 GAGCAGGGCCATAATTAT 69


RESULT 6
AR207283/c
LOCUS       AR207283                2179 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 1 from patent US 6372711.
ACCESSION   AR207283
VERSION     AR207283.1  GI:21506147
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2179)
  AUTHORS   Kelton,C.Ann., Cheng,S.Vui.Yen., Nugent,N.Patrice. and
            Schweickhardt,R.Lynn.
  TITLE     Methods for assaying human FSH using human FSH receptor
  JOURNAL   Patent: US 6372711-A 1 16-APR-2002;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         86 GAGCAGGGCCATAATTAT 69


RESULT 7
S59900/c
LOCUS       S59900                  2179 bp    mRNA    linear   PRI 23-JUL-1993
DEFINITION  follicle stimulating hormone receptor [human, testis, mRNA, 2179
            nt].
ACCESSION   S59900
VERSION     S59900.1  GI:300072
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2179)
  AUTHORS   Kelton,C.A., Cheng,S.V., Nugent,N.P., Schweickhardt,R.L.,
            Rosenthal,J.L., Overton,S.A., Wands,G.D., Kuzeja,J.B.,
            Luchette,C.A. and Chappel,S.C.
  TITLE     The cloning of the human follicle stimulating hormone receptor and
            its expression in COS-7, CHO, and Y-1 cells
  JOURNAL   Mol. Cell. Endocrinol. 89 (1-2), 141-151 (1992)
  PUBMED    1301382
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 130880] from the original journal article.
FEATURES             Location/Qualifiers
     source          1. .2179
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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     CDS             75. .2162
                     /gene="follicle stimulating hormone receptor, FSH
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                     DTRIAKRMAMLIFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLFHPINSCANPF
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
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Db         86 GAGCAGGGCCATAATTAT 69


RESULT 8
HUMFSHREC/c
LOCUS       HUMFSHREC               2186 bp    mRNA    linear   PRI 08-NOV-1994
DEFINITION  H.sapiens follicle stimulating hormone receptor mRNA, complete cds.
ACCESSION   M95489
VERSION     M95489.1  GI:182772
KEYWORDS    G-protein coupled receptor; follicle stimulating hormone (FSH)
            receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2186)
  AUTHORS   Tilly,L.T., Aihara,T., Nishimori,K., Jai,X., Billig,H.,
            Kowalski,K.I., Perlas,E.A. and Hsueh,A.J.W.
  TITLE     Expression of recombinant human follicle-stimulating hormone
            receptor: Species-specific ligand binding, signal transduction, and
            identification of multiple ovarian messenger ribonucleic acid
            transcripts
  JOURNAL   Endocrinology (1992) In press
COMMENT     Original source text: Homo sapiens male adult testis cDNA to mRNA.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 18;  DB 8;  Length 2186;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
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Db         87 GAGCAGGGCCATAATTAT 70


RESULT 9
A76125/c
LOCUS       A76125                2222 bp    DNA     linear   PAT 19-OCT-1999
DEFINITION  Sequence 1 from Patent WO9320199.
ACCESSION   A76125
VERSION     A76125.1  GI:6088261
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2222)
  AUTHORS   Dijkema,R. and De,L.R.
  TITLE     HUMAN GONADOTROPIN RECEPTOR (FSH RECEPTOR)
  JOURNAL   Patent: WO 9320199-A 1 14-OCT-1993;
            AKZO NV (NL); DIJKEMA REIN (NL)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.6;
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Qy          1 GAGCAGGGCCATAATTAT 18
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Db         96 GAGCAGGGCCATAATTAT 79


RESULT 10
CQ715054/c
LOCUS       CQ715054              2374 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 988 from Patent WO02068579.
ACCESSION   CQ715054
VERSION     CQ715054.1  GI:42275911
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 988 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .2374
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                     /mol_type="unassigned DNA"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         79 GAGCAGGGCCATAATTAT 62


RESULT 11
AR270646/c
LOCUS       AR270646              2393 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 1209 from patent US 6500938.
ACCESSION   AR270646
VERSION     AR270646.1  GI:29701880
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2393)
  AUTHORS   Au-Young,J. and Seilhamer,J.J.
  TITLE     Composition for the detection of signaling pathway gene expression
  JOURNAL   Patent: US 6500938-A 1209 31-DEC-2002;
            Incyte Genomics, Inc.; Palo Alto, CA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .2393
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 2393;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
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  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         78 GAGCAGGGCCATAATTAT 61


RESULT 12
AX548836/c
LOCUS       AX548836               2393 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 121 from Patent WO02061087.
ACCESSION   AX548836
VERSION     AX548836.1  GI:25813727
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE     Antigenic peptides, such as for G protein-coupled receptors
            (GPCRs), antibodies thereto, and systems for identifying such
            antigenic peptides
  JOURNAL   Patent: WO 02061087-A 121 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2393
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 6;  Length 2393;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         78 GAGCAGGGCCATAATTAT 61


RESULT 13
HUMFSHRE/c
LOCUS       HUMFSHRE               2393 bp    mRNA    linear   PRI 12-JAN-2005
DEFINITION  Human follicle stimulating hormone receptor mRNA, complete cds.
ACCESSION   M65085
VERSION     M65085.1  GI:182770
KEYWORDS    follicle stimulating hormone (FSH) receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 2393)
  AUTHORS   Minegishi,T., Nakamura,K., Takakura,Y., Ibuki,Y., Igarashi,M. and
            Minegishi,T.
  TITLE     Cloning and sequencing of human FSH receptor cDNA
  JOURNAL   Biochem. Biophys. Res. Commun. 175 (3), 1125-1130 (1991)
   PUBMED   1709010
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .2393
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="Unassigned"
     gene            1. .2393
                     /gene="FSHR"
     CDS             67. .2154
                     /gene="FSHR"
                     /codon_start=1
                     /product="follicle stimulating hormone receptor"
                     /protein_id="AAA52477.1"
                     /db_xref="GI:182771"
                     /db_xref="GDB:G00-127-510"
                     /translation="MALLLVSLLAFLSLGSGCHHRICHCSNRVFLCQESKVTEIPSDL
                     PRNAIELRFVLTKLRVIQKGAFSGFGDLEKIEISQNDVLEVIEADVFSNLPKLHEIRI
                     EKANNLLYITPEAFQNLPNLQYLLISNTGIKHLPDVHKIHSLQKVLLDIQDNINIHTI
                     ERNSFVGLSFESVILWLNKNGIQEIHNCAFNGTQLDAVNLSDNNNLEELPNDVFHGAS
                     GPVILDISRTRIHSLPSYGLENLKKLRARSTYNLKKLPTLEKLVALMEASLTYPSHCC
                     AFANWRRQISELHPICNKSILRQEVDYMTQARGQRSSLAEDNESSYSRGFDMTYTEFD
                     YDLCNEVVDVTCSPKPDAFNPCEDIMGYNILRVLIWFISILAITGNIIVLVILTTSQY
                     KLTVPRFLMCNLAFADLCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTV
                     FASELSVYTLTAITLERWHTITHAMQLDCKVQLRHAASVMVMGWIFAFAAALFPIFGI
                     SSYMKVSICLPMDIDSPLSQLYVMSLLVLNVLAFVVICGCYIHIYLTVRNPNIVSSSS
                     DTRIAKRMAMLIFTDFLCMAPISFFAISASLKVPLITVSKAKILLVLFHPINSCANPF
                     LYAIFTKNFRRDFFILLSKCGCYEMQAQIYRTETSSTVHNTHPRNGHCSSAPRVTSGS
                     TYILVPLSHLAQN"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 8;  Length 2393;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         78 GAGCAGGGCCATAATTAT 61


RESULT 14
AC092533
LOCUS       AC092533             121688 bp    DNA     linear   PRI 15-APR-2005
DEFINITION  Homo sapiens BAC clone RP11-57I10 from 2, complete sequence.
ACCESSION   AC092533 AC027148
VERSION     AC092533.1  GI:14718373
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 121688)
  AUTHORS   Haakenson,W. and Shah,N.
  TITLE     The sequence of Homo sapiens BAC clone RP11-57I10
  JOURNAL   Unpublished (2001)
REFERENCE   2  (bases 1 to 121688)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   3  (bases 1 to 121688)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUL-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 121688)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2002) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE   5  (bases 1 to 121688)
  AUTHORS   Wilson,R.K.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-2005) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Jul 14, 2001 this sequence version replaced gi:7622375.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu
                Contact: submissions@watson.wustl.edu
            -------------- Summary Statistics
```

```
            Center project name: H_NH0057I10
            Drafting Center: WIBR
          --------------.

          NOTICE:

          This sequence was finished as follows unless otherwise noted:
          all regions were double stranded, sequenced with an alternate
          chemistry, or covered by high quality data (i.e., phred quality >=
          30); an attempt was made to resolve all sequencing problems, such
          as compressions and repeats; all regions were covered by sequence
          from more than one subclone; and the assembly was confirmed by
          restriction digest.

          MAPPING INFORMATION:
          Mapping information for this clone was provided by Dr. Wes Warren,
          Department of Genetics, Washington University, St. Louis MO. For
          additional information about the map position of this sequence, see
          http://genome.wustl.edu

          SOURCE INFORMATION:
          The RPCI-11 human BAC library was made from the blood of one male
          donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
          Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
          approach for construction of bacterial artificial chromosome
          libraries. Genomics 51:1-8. The clone may be obtained either from
          Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
          and coworkers at http://www.chori.org
          VECTOR:  pBACe3.6

          NEIGHBORING SEQUENCE INFORMATION:
          The clone sequenced to the left is RP11-125F24, 2000 bp overlap.
          Actual start of this clone is at base position 9748 of RP11-125F24;
          actual end is at base position 121688 of RP11-57I10.

          The sequence of AC027148 has been incorporated into AC092533.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /clone="RP11-57I10"
                     /clone_lib="RPCI-11"
     gene            complement(82833. .83058)
                     /gene="FSHR"
     mRNA            complement(82833. .83058)
                     /gene="FSHR"
     CDS             complement(<82833. .82984)
                     /gene="FSHR"
                     /note="Homo sapiens follicle stimulating hormone receptor
                     (FSHR), transcript variant 1, mRNA.; H_NH0057I10.1
                     This gene was based on gi(31657137)
                     Continues as H_NH0125F24.1"
                     /codon_start=1
                     /product="unknown"
                     /protein_id="AAX88895.1"
                     /db_xref="GI:62630150"
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                     PRNAIEL"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 8;  Length 121688;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
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Db      82973 GAGCAGGGCCATAATTAT 82990


RESULT 15
AC083827
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```
LOCUS       AC083827              158709 bp    DNA     linear   HTG 24-JAN-2002
DEFINITION  Homo sapiens chromosome 2 clone RP11-345C21, WORKING DRAFT
            SEQUENCE, 23 unordered pieces.
ACCESSION   AC083827
VERSION     AC083827.2  GI:15375221
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 158709)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 158709)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-OCT-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Aug 30, 2001 this sequence version replaced gi:10445290.

            ------------------- Genome Center --------------------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            Contact: submissions@watson.wustl.edu
            ---------------- Project Information -----------------
            Center project name: H_NH0345C21
            ------------------------------------------------------
            -------------- Summary Statistics  --------------
            Sequencing vector: M13; 100%
            Sequencing vector: plasmid; 0%
            Chemistry: Dye-primer ET; 8% of reads
            Chemistry: Dye-terminator Big Dye; 92% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 142571 bases at least Q40
            Consensus quality: 147681 bases at least Q30
            Consensus quality: 150874 bases at least Q20
            Insert size: 167000; agarose-fp
            Insert size: 156781; sum-of-contigs
            Quality coverage: 3.10 in Q20 bases; agarose-fp
            Quality coverage: 3.36 in Q20 bases; sum-of-contigs
            ------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 23 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1192: contig of 1192 bp in length
            *     1193     1292: gap of unknown length
            *     1293     2772: contig of 1480 bp in length
            *     2773     2872: gap of unknown length
            *     2873     4401: contig of 1529 bp in length
            *     4402     4501: gap of unknown length
            *     4502     6753: contig of 2252 bp in length
            *     6754     6853: gap of unknown length
            *     6854     8763: contig of 1910 bp in length
            *     8764     8863: gap of unknown length
            *     8864    11063: contig of 2200 bp in length
            *    11064    11163: gap of unknown length
            *    11164    14152: contig of 2989 bp in length
            *    14153    14252: gap of unknown length
            *    14253    17321: contig of 3069 bp in length
            *    17322    17421: gap of unknown length
            *    17422    19872: contig of 2451 bp in length
            *    19873    19972: gap of unknown length
            *    19973    22886: contig of 2914 bp in length
            *    22887    22986: gap of unknown length
```

```
            *    22987    26989: contig of 4003 bp in length
            *    26990    27089: gap of unknown length
            *    27090    31373: contig of 4284 bp in length
            *    31374    31473: gap of unknown length
            *    31474    36312: contig of 4839 bp in length
            *    36313    36412: gap of unknown length
            *    36413    41598: contig of 5186 bp in length
            *    41599    41698: gap of unknown length
            *    41699    49543: contig of 7845 bp in length
            *    49544    49643: gap of unknown length
            *    49644    56734: contig of 7091 bp in length
            *    56735    56834: gap of unknown length
            *    56835    66438: contig of 9604 bp in length
            *    66439    66538: gap of unknown length
            *    66539    76934: contig of 10396 bp in length
            *    76935    77034: gap of unknown length
            *    77035    88008: contig of 10974 bp in length
            *    88009    88108: gap of unknown length
            *    88109   101914: contig of 13806 bp in length
            *   101915   102014: gap of unknown length
            *   102015   117937: contig of 15923 bp in length
            *   117938   118037: gap of unknown length
            *   118038   133609: contig of 15572 bp in length
            *   133610   133709: gap of unknown length
            *   133710   158709: contig of 25000 bp in length.
FEATURES             Location/Qualifiers
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                     /note="assembly_name:Contig27"
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                     /note="assembly_name:Contig28"
ORIGIN

  Query Match             100.0%;  Score 18;  DB 14;  Length 158709;
  Best Local Similarity   100.0%;  Pred. No. 5.6;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db      35240 GAGCAGGGCCATAATTAT 35257


Search completed: November 29, 2005, 23:42:24
Job time : 898.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 29, 2005, 18:22:32 ; Search time 223.5 Seconds
(without alignments)
536.754 Million cell updates/sec

Title: US-10-018-716B-1
Perfect score: 18
Sequence: 1 gagcagggccataattat 18

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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8: geneseqn2003as:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	18	100.0	18	4	AAC90409	Aac90409 Human FSH
	2	18	100.0	18	4	AAC90408	Aac90408 Human FSH
c	3	18	100.0	1922	11	ADP03559	Adp03559 Human GPC
c	4	18	100.0	2019	10	ADC24202	Adc24202 Human NOV
c	5	18	100.0	2179	2	AAT63181	Aat63181 FSH recep
c	6	18	100.0	2180	2	AAQ29377	Aaq29377 FSHR DNA.
c	7	18	100.0	2222	2	AAQ50013	Aaq50013 FSH recep
c	8	18	100.0	2393	8	ABZ42665	Abz42665 Human fol
c	9	18	100.0	2393	10	ADD25503	Add25503 Binding d
c	10	18	100.0	2393	10	ACA56611	Aca56611 Human sig
c	11	18	100.0	2393	12	ADI56407	Adi56407 Human pol
c	12	18	100.0	2393	12	ADO29879	Ado29879 Human GPC
	13	15	83.3	507	13	ADR26224	Adr26224 Breast ca
c	14	15	83.3	612	6	ABT03390	Abt03390 Ovary cel
c	15	15	83.3	628	6	ABT03391	Abt03391 Ovary cel
	16	15	83.3	2021	13	ADT19293	Adt19293 Plant cDN
c	17	15	83.3	3659	4	ABL12007	Abl12007 Drosophil
	18	15	83.3	8253	13	ADR84405	Adr84405 Aspergill
c	19	15	83.3	9140	4	ABL12006	Abl12006 Drosophil
	20	15	83.3	76829	14	AEA61117	Aea61117 Human FLJ
c	21	15	83.3	180227	13	ABD33268	Abd33268 Human can
c	22	15	83.3	202251	11	ACN44504	Acn44504 Mouse gen
	23	14	77.8	400	14	AEB67475	Aeb67475 Rice geno
	24	14	77.8	574	11	ADT97777	Adt97777 Colon can
	25	14	77.8	574	11	ADX44259	Adx44259 Human cDN
	26	14	77.8	810	8	ACA36201	Aca36201 Prokaryot
c	27	14	77.8	900	11	ABD01221	Abd01221 Klebsiell
c	28	14	77.8	975	13	ADT45042	Adt45042 Bacterial
c	29	14	77.8	1059	5	AAH65707	Aah65707 C glutami
c	30	14	77.8	1149	4	AAF67932	Aaf67932 Corynebac
c	31	14	77.8	1200	14	ADZ62987	Adz62987 Murine Hs
c	32	14	77.8	1254	13	ADS59283	Ads59283 Bacterial
	33	14	77.8	1506	13	ADS48503	Ads48503 Bacterial
	34	14	77.8	1617	5	AAS93640	Aas93640 DNA encod
	35	14	77.8	1887	4	AAI58166	Aai58166 Human pol
	36	14	77.8	1887	5	ADQ98372	Adq98372 DNA encod
	37	14	77.8	1887	9	ADB48132	Adb48132 Novel hum
	38	14	77.8	1887	13	ADS47940	Ads47940 Bacterial
	39	14	77.8	1903	4	AAH17958	Aah17958 Human cDN
c	40	14	77.8	2450	10	ADB68874	Adb68874 C. neofor
c	41	14	77.8	2975	6	AAD29106	Aad29106 Human MDM
c	42	14	77.8	3678	2	AAQ53996	Aaq53996 Equine he
c	43	14	77.8	3678	2	AAX38299	Aax38299 Equine he
	44	14	77.8	3762	11	ACH99131	Ach99131 Klebsiell
	45	14	77.8	4262	2	AAT38484	Aat38484 Rat petri

ALIGNMENTS

RESULT 1
AAC90409/c
ID AAC90409 standard; RNA; 18 BP.
XX
AC AAC90409;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human FSH receptor specific antisense oligonucleotide #2.
XX
KW Human; cytostatic; follicle-stimulating hormone receptor; FSHR;
KW fertility; menstrual cycle; chemopreventive; chemotherapy; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200073416-A1.
XX
PD 07-DEC-2000.
XX
PF 16-MAY-2000; 2000WO-US013488.
XX
PR 28-MAY-1999; 99US-0136489P.
PR 08-OCT-1999; 99US-0158612P.
XX
PA (UYCI-) UNIV CINCINNATI.
XX
PI Labarbera AR, Zhu C, Wang Y;
XX
DR WPI; 2001-091069/10.
XX
PT New composition for regulating fertility, and for chemoprevention and
PT chemotherapy of cancer, comprises an antisense oligonucleotide that is
PT complementary to a nucleotide sequence of a follicle-stimulating hormone
PT receptor.
XX
PS Claim 13; Page 29; 89pp; English.
XX
CC The present invention relates to a composition, which comprises at least
CC one antisense oligonucleotide that is complementary to follicle-
CC stimulating hormone receptor (FSHR) coding sequence. The present sequence
CC is one such oligonucleotide used in the composition. The composition of
CC the present invention can be used for regulating hormones of a host. The

```
CC   composition is also useful for regulating fertility and menstrual cycle.
CC   In addition, the composition is useful as a chemopreventive or
CC   chemotherapy for cancers (e.g. breast, bladder, cervix, lung, liver,
CC   ovary, colon, stomach, or especially ovarian cancers), gestational
CC   trophoblastic tumours or testicular germ cell tumours
XX
SQ   Sequence 18 BP; 4 A; 5 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         18 GAGCAGGGCCATAATTAT 1


RESULT 2
AAC90408
ID   AAC90408 standard; DNA; 18 BP.
XX
AC   AAC90408;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human FSH receptor specific antisense oligonucleotide #1.
XX
KW   Human; cytostatic; follicle-stimulating hormone receptor; FSHR;
KW   fertility; menstrual cycle; chemopreventive; chemotherapy; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073416-A1.
XX
PD   07-DEC-2000.
XX
PF   16-MAY-2000; 2000WO-US013488.
XX
PR   28-MAY-1999;   99US-0136489P.
PR   08-OCT-1999;   99US-0158612P.
XX
PA   (UYCI-) UNIV CINCINNATI.
XX
PI   Labarbera AR,  Zhu C,  Wang Y;
XX
DR   WPI; 2001-091069/10.
XX
PT   New composition for regulating fertility, and for chemoprevention and
PT   chemotherapy of cancer, comprises an antisense oligonucleotide that is
PT   complementary to a nucleotide sequence of a follicle-stimulating hormone
PT   receptor.
XX
PS   Claim 13; Page 29; 89pp; English.
XX
CC   The present invention relates to a composition, which comprises at least
CC   one antisense oligonucleotide that is complementary to follicle-
CC   stimulating hormone receptor (FSHR) coding sequence. The present sequence
CC   is one such oligonucleotide used in the composition. The composition of
CC   the present invention can be used for regulating hormones of a host. The
CC   composition is also useful for regulating fertility and menstrual cycle.
CC   In addition, the composition is useful as a chemopreventive or
CC   chemotherapy for cancers (e.g. breast, bladder, cervix, lung, liver,
CC   ovary, colon, stomach, or especially ovarian cancers), gestational
CC   trophoblastic tumours or testicular germ cell tumours
XX
SQ   Sequence 18 BP; 6 A; 3 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.2;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db          1 GAGCAGGGCCATAATTAT 18


RESULT 3
ADP03559/c
ID   ADP03559 standard; DNA; 1922 BP.
XX
AC   ADP03559;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human GPCR follicle stimulating hormone receptor variant "Gene 4" DNA.
XX
KW   GPCR; G-protein coupled receptor; neuroprotective; nootropic;
KW   tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant;
KW   anticonvulsant; antiparkinsonian; cytostatic; cardiant; hypotensive;
KW   antianginal; analgesic; anorectic; anti-HIV; antiasthmatic; osteopathic;
KW   uropathic; antiulcer; antiallergic; cell cycle regulation; neurological;
KW   severe mental retardation; dyskinesia; brain; spinal cord; affective;
KW   neoplastic; cardiovascular; immunological; immune; endocrinal; growth;
KW   eating; HIV infection; cancer; metabolic; pituitary;
KW   chromosome identification; gene therapy; human; ds; gene;
KW   follicle stimulating hormone; FSH receptor variant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             17. .1753
FT                   /*tag=  a
FT                   /product= "Human GPCR follicle stimulating hormone
FT                   receptor variant "Gene 4" protein"
XX
PN   WO2003062393-A2.
XX
PD   31-JUL-2003.
XX
PF   22-JAN-2003; 2003WO-US001911.
XX
PR   22-JAN-2002; 2002US-0350724P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Ramanathan CS,  Gopal S,  Mintier G,  Feder JN;
XX
DR   WPI; 2003-618283/58.
DR   P-PSDB; ADP03570.
XX
PT   New nucleic acid molecule encoding a human G-protein coupled receptor,
PT   useful for diagnosing, preventing or treating diseases involving the
PT   receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
PT   cancer.
XX
PS   Claim 1; SEQ ID NO 4; 224pp; English.
XX
CC   The invention relates to a novel isolated GPCR (G-protein coupled
CC   receptor) nucleic acid molecule. The polynucleotide and polypeptide of
CC   the invention demonstrate neuroprotective, nootropic, tranquiliser,
CC   antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,
CC   antiparkinsonian, cytostatic, cardiant, hypotensive, antianginal,
CC   analgesic, anorectic, anti-HIV, antiasthmatic, osteopathic, uropathic,
CC   antiulcer and antiallergic properties. The nucleic acid molecule and
CC   polypeptide of the invention may be useful in diagnosing, preventing,
CC   treating or ameliorating a medical condition, such as a disorder related
CC   to aberrant G-protein coupled signalling, a disorder related to aberrant
CC   cell cycle regulation, neurological disorders, severe mental retardation
CC   and dyskinesias, brain disorders, spinal cord disorders, affective
CC   disorders, neoplastic disorders, cardiovascular disorders, immunological
CC   disorders, immune-related disorders, endocrinal diseases, growth
CC   disorders, eating disorders, HIV infection, cancers, metabolic disorders
CC   and pituitary disorders. Furthermore, the polynucleotide may be used in
CC   chromosome identification, in identifying organisms from minute
CC   biological samples, in gene therapy or as a molecular weight marker. The
CC   current sequence is that of a human GPCR (G-protein coupled receptor) DNA
```

```
CC   which was isolated by the method of the invention.
XX
SQ   Sequence 1922 BP; 499 A; 504 C; 387 G; 532 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 11;  Length 1922;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         28 GAGCAGGGCCATAATTAT 11


RESULT 4
ADC24202/c
ID   ADC24202 standard; cDNA; 2019 BP.
XX
AC   ADC24202;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human NOV3a encoding cDNA SEQ ID NO:9.
XX
KW   human; NOVX; cardiant; antiarteriosclerotic; hypotensive; vasotropic;
KW   dermatological; anorectic; immunosuppressive; cytostatic;
KW   antiinfertility; haemostatic; anti-HIV; antiasthmatic; antiinflammatory;
KW   neuroprotective; anabolic; nootropic; antiparkinsonian; gene therapy;
KW   cardiomyopathy; atherosclerosis; hypertension; congenital heart defect;
KW   pulmonary stenosis; scleroderma; obesity; metabolic disturbance; obesity;
KW   transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;
KW   prostate cancer; diabetes; metabolic disorder; neoplasm; adenocarcinoma;
KW   fertility; haemophilia; graft versus host disease; AIDS;
KW   bronchial asthma; Crohn's disease; multiple sclerosis;
KW   infectious disease; anorexia; neurodegenerative disorder;
KW   Alzheimer's disease; Parkinson's disease; immune disorder;
KW   haematopoietic disorder; dyslipidaemia; wasting disorder; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             61. .1962
FT                   /*tag=  a
FT                   /product= "NOV3a"
XX
PN   WO2003076584-A2.
XX
PD   18-SEP-2003.
XX
PF   06-MAR-2003; 2003WO-US006951.
XX
PR   06-MAR-2002; 2002US-0361974P.
PR   19-MAR-2002; 2002US-0365477P.
PR   22-MAR-2002; 2002US-0366928P.
PR   06-AUG-2002; 2002US-0401661P.
PR   05-MAR-2003; 2003US-00401661.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Alsobrook JP,  Burgess CE,  Edinger SR,  Gerlach VL,  Ji W,  Kekuda R;
PI   Li L,  Macdougall JR,  Miller CE,  Millet I,  Patturajan M,  Pena CEA;
PI   Rieger DK,  Sciore P,  Shenoy SG,  Smithson G,  Spytek KA,  Stone DJ;
PI   Voss EZ,  Zhong M;
XX
DR   WPI; 2003-722330/68.
DR   P-PSDB; ADC24203.
XX
PT   New NOVX polypeptides and nucleic acids, useful for diagnosing or
PT   treating e.g. cardiomyopathy, atherosclerosis, hypertension, scleroderma,
PT   obesity, prostate cancer, AIDS, bronchial asthma, Crohn's disease, or
PT   multiple sclerosis.
XX
PS   Claim 20; SEQ ID NO 9; 229pp; English.
XX
CC   The present invention describes novel human proteins, designated NOVX
CC   proteins. The NOVX sequences have cardiant, antiarteriosclerotic,
CC   hypotensive, vasotropic, dermatological, anorectic, immunosuppressive,
CC   cytostatic, antiinfertility, haemostatic, anti-HIV, antiasthmatic,
CC   antiinflammatory, neuroprotective, anabolic, nootropic and
CC   antiparkinsonian activities, and can be used in gene therapy. The NOVX
CC   sequences can be used as a therapeutic in the manufacture of a medicament
CC   for treating a syndrome associated with a human disease, such as a
CC   pathology associated with NOVX. The NOVX proteins and nucleic acids
CC   encoding them are useful for diagnosing or treating pathologies, diseases
CC   or conditions associated with NOVX sequences, including cardiomyopathy,
CC   atherosclerosis, hypertension, congenital heart defects, pulmonary
CC   stenosis, scleroderma, obesity, metabolic disturbances associated with
CC   obesity, transplantation, adrenoleukodystrophy, congenital adrenal
CC   hyperplasia, prostate cancer, diabetes, metabolic disorders, neoplasm,
CC   adenocarcinoma, fertility, haemophilia, graft versus host disease, AIDS,
CC   bronchial asthma, Crohn's disease, multiple sclerosis, infectious
CC   disease, anorexia, neurodegenerative disorders (e.g. Alzheimer's disease,
CC   or Parkinson's disease), immune disorders, haematopoietic disorders,
CC   dyslipidaemias, and wasting disorders associated with chronic diseases.
CC   The proteins can also be used as immunogens to produce antibodies and as
CC   vaccines. The sequences may further be used in chromosome mapping,
CC   identifying individual from minute biological samples (tissue typing),
CC   and in forensic identification of a biological sample. The present
CC   sequence encodes human NOV3a from the present invention.
XX
SQ   Sequence 2019 BP; 527 A; 514 C; 411 G; 567 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 10;  Length 2019;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         72 GAGCAGGGCCATAATTAT 55


RESULT 5
AAT63181/c
ID   AAT63181 standard; DNA; 2179 BP.
XX
AC   AAT63181;
XX
DT   20-JUN-1997  (first entry)
XX
DE   FSH receptor gene wild-type allele.
XX
KW   Follicle stimulating hormone receptor; FSH receptor; ovarian dysgenesis;
KW   hypergonadotropic hypogonadism; diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   exon            70. .227
FT                   /*tag=  c
FT                   /note= "nucleotides 70-227 correspond to nucleotides 1-
FT                   158 of fshr exon 1"
FT   CDS             75. .2159
FT                   /*tag=  a
FT   exon            228. .298
FT                   /*tag=  c
FT                   /note= "nucleotides 228-298 correspond to nucleotides 7-
FT                   77 of fshr exon 2"
FT   exon            299. .373
FT                   /*tag=  c
FT                   /note= "nucleotides 299-373 correspond to nucleotides 6-
FT                   80 of fshr exon 3"
FT   exon            374. .450
FT                   /*tag=  c
FT                   /note= "nucleotides 374-450 correspond to nucleotides 6-
FT                   82 of fshr exon 4"
FT   exon            451. .520
FT                   /*tag=  c
```

```
FT                   /note= "nucleotides 451-520 correspond to nucleotides 8-
FT                   77 of fshr exon 5"
FT   exon            521. .598
FT                   /*tag=  c
FT                   /note= "nucleotides 521. .598 correspond to nucleotides 6-
FT                   83 of fshr exon 6"
FT   exon            599. .668
FT                   /*tag=  c
FT                   /note= "nucleotides 599-668 correspond to nucleotides 6-
FT                   75 of fshr exon 7"
FT   mutation        640
FT                   /*tag=  b
FT                   /note= "a C to T mutation in codon 189 correlates with
FT                   ovarian dysgenesis"
FT   exon            669. .742
FT                   /*tag=  c
FT                   /note= "nucleotides 669-742 correspond to nucleotides 7-
FT                   80 of fshr exon 8"
FT   exon            743. .928
FT                   /*tag=  c
FT                   /note= "nucleotides 743-928 correspond to nucleotides 6-
FT                   191 of fshr exon 9"
FT   exon            929. .2179
FT                   /*tag=  c
FT                   /note= "nucleotides 929-2179 correspond to nucleotides
FT                   102-1352 of fshr exon 10"
XX
PN   WO9711194-A1.
XX
PD   27-MAR-1997.
XX
PF   20-SEP-1996;   96WO-FI000501.
XX
PR   20-SEP-1995;   95US-00531070.
XX
PA   (UYHE-) UNIV HELSINKI LICENSING LTD OY.
XX
PI   De La Chapelle A,  Aittomaeki K,  Huhtaniemi I;
XX
DR   WPI; 1997-202900/18.
DR   P-PSDB; AAW14782.
XX
PT   Diagnosis of ovarian dysgenesis and carriers from DNA abnormalities - by
PT   amplifying DNA including follicle stimulating hormone receptor allele(s),
PT   i.e. codon 189, cleaving fragments, and examination.
XX
PS   Claim 17; Page 18-21; 43pp; English.
XX
CC   A DNA sequence (AAT63181) comprises the coding region from exons 1-10 of
CC   the wild-type fshr gene that codes for human follicle stimulating hormone
CC   (FSH) receptor (AAW14782). A C to T mutation in exon 7 (codon 189) is
CC   associated with ovarian dysgenesis. In a method for determining a FSH
CC   receptor genotype in a human patient, fshr exon 7, or a portion of it, is
CC   isolated by PCR amplification (see also AAT63195-96) and exposed to BsmI.
CC   Exon 7 contains a unique BsmI site which, if mutated, will produce no
CC   BsmI digestion products, thereby enabling diagnosis of ovarian dysgenesis
XX
SQ   Sequence 2179 BP; 575 A; 561 C; 444 G; 599 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 2;  Length 2179;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         86 GAGCAGGGCCATAATTAT 69


RESULT 6
AAQ29377/c
ID   AAQ29377 standard; DNA; 2180 BP.
XX
AC   AAQ29377;
XX
DT   25-MAR-2003  (revised)
DT   04-MAR-1993  (first entry)
XX
DE   FSHR DNA.
XX
KW   Human; follicle stimulating hormone receptor; maturation;
KW   spermatogenesis; birth control; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             75. .2159
FT                   /*tag=  a
FT   sig_peptide     75. .126
FT                   /*tag=  b
FT   mat_peptide     127. .2159
FT                   /*tag=  c
XX
PN   WO9216620-A1.
XX
PD   01-OCT-1992.
XX
PF   02-JAN-1992;   92WO-US000122.
XX
PR   15-MAR-1991;   91US-00670085.
XX
PA   (ISTF ) ARS APPL RES SYST HOLDING NV.
XX
PI   Kelton CA,  Cheng SVY,  Nugent NP,  Schweickhardt RL;
XX
DR   WPI; 1992-349206/42.
DR   P-PSDB; AAR29377.
XX
PT   Pure human FSH receptor, fragments and mutants - for preventing follicle
PT   growth, maturation and spermatogenesis, also for use of appropriate cell
PT   lines for bio-assays of FSH.
XX
PS   Claim 7; Page 25; 48pp; English.
XX
CC   The DNA sequence encoding human follicle stimulating hormone receptor
CC   (FSHR) was obtd. by screening a lambda gt11 cDNA library constructed from
CC   RNA extracted from human testis and amplified, with a rat FSHR cDNA clone
CC   as a probe. Positive colonies were used for a secondary screen which
CC   isolated five putative human FSHR clones. None of the clones contained
CC   the complete hFSHR coding region but could be overlapped using GCG to
CC   give the complete sequence. hFSHR binds to FSH to reduce endogenous FSH
CC   bioactivity, in females to prevent follicle growth and maturation and in
CC   males to prevent spermatogenesis, i.e. as a birth control agent. (Updated
CC   on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 2180 BP; 577 A; 560 C; 444 G; 599 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 2;  Length 2180;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         87 GAGCAGGGCCATAATTAT 70


RESULT 7
AAQ50013/c
ID   AAQ50013 standard; cDNA to mRNA; 2222 BP.
XX
AC   AAQ50013;
XX
DT   25-MAR-2003  (revised)
DT   05-MAY-1994  (first entry)
XX
DE   FSH receptor.
XX
```

```
KW   FSH; receptor; follicle stimulating hormone; GST;
KW   glutathione-S-transferase; primer; PCR; amplification;
KW   polymerase chain reaction; probe; antibody; overstimulation; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             85. .2172
FT                   /*tag= a
FT                   /product= "FSH_receptor"
FT   primer_bind     136. .151
FT                   /*tag= b
FT                   /note= "first primer for GST-FSH-R1 and for GST-FSH-R2"
FT   primer_bind     763. .776
FT                   /*tag= d
FT                   /note= "primer for GST-FSH-R3"
FT   primer_bind     complement(770. .787)
FT                   /*tag= f
FT                   /note= "primer for GST-FSH-R2"
FT   primer_bind     complement(1167. .1183)
FT                   /*tag= e
FT                   /note= "primer for GST-FSH-R1 and for GST-FSH-R3"
FT   primer_bind     1168. .1183
FT                   /*tag= c
FT                   /note= "primer for GST-FSH-R3"
XX
PN   WO9320199-A1.
XX
PD   14-OCT-1993.
XX
PF   29-MAR-1993;   93WO-EP000780.
XX
PR   30-MAR-1992;   92EP-00200886.
XX
PA   (ALKU ) AKZO NV.
XX
PI   Dijkema R,  De Leeuw R;
XX
DR   WPI; 1993-336907/42.
DR   P-PSDB; AAR42082.
XX
PT   New follicle stimulating hormone receptor - and derived antibodies, anti-
PT   idiotypic antibodies, and transfected cells, useful e.g. in diagnosis and
PT   as antidote for FSH overstimulation.
XX
PS   Disclosure; Page 20-23; 42pp; English.
XX
CC   The primers given in AAQ50029-34 were used in the cloning of GST-FSH- R1,
CC   GST-FSH-R2 and GST-FSH-R3 fusion protein constructs. Screening of the
CC   human testis cDNA library with a hFSH-R specific probe resulted in five
CC   recombinant phages positive in hybridisation. Sequence analysis was
CC   performed of the 2222 bp fragment of pGEM3Zc1 (AAQ50013). (Updated on 25-
CC   MAR-2003 to correct PN field.)
XX
SQ   Sequence 2222 BP; 598 A; 565 C; 453 G; 606 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 2;  Length 2222;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         96 GAGCAGGGCCATAATTAT 79


RESULT 8
ABZ42665/c
ID   ABZ42665 standard; DNA; 2393 BP.
XX
AC   ABZ42665;
XX
DT   04-MAR-2003  (first entry)
XX
DE   Human follicle stimulating hormone receptor nucleotide SEQ ID NO:121.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200261087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
XX
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC,  Roush CL,  Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   P-PSDB; ABP81819.
XX
PT   New isolated antigenic peptides e.g., for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 1; 523pp; English.
XX
CC   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific
CC   antibodies. The peptides and antibodies are also useful for detecting the
CC   presence or absence of corresponding GPCRs. The antigenic peptides for
CC   GPCRs and antibodies are useful for diagnosing and designing drugs for
CC   treating immune-related diseases, growth-related diseases, cell
CC   regeneration-related disease, immunological-related cell proliferative
CC   diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC   atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC   osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC   inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC   disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC   anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC   loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC   hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC   any other disorder in which GPCRs are involved. The antibodies may be
CC   used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 18;  DB 8;  Length 2393;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         78 GAGCAGGGCCATAATTAT 61
```

RESULT 9
ADD25503/c
ID ADD25503 standard; DNA; 2393 BP.
XX
AC ADD25503;
XX
DT 15-JAN-2004 (first entry)
XX
DE Binding domain-immunoglobulin fusion protein-associated DNA #36.
XX
KW ds; Binding domain; immunoglobulin; fusion protein; cytostatic;
KW antiarthritic; immunosuppressive; antidiabetic; antithyroid;
KW neuroprotective; hinge region; immunoglobulin heavy chain;
KW CH2 constant region; CH3 constant region; IgG1;
KW antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
KW malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
KW rheumatoid arthritis; myasthenia gravis; Grave's disease;
KW type I diabetes mellitus; multiple sclerosis; autoimmune disease.
XX
OS Unidentified.
XX
PN US2003118592-A1.
XX
PD 26-JUN-2003.
XX
PF 25-JUL-2002; 2002US-00207655.
XX
PR 17-JAN-2001; 2001US-0367358P.
PR 17-JAN-2002; 2002US-00053530.
PR 03-JUN-2002; 2002US-0385691P.
XX
PA (GENE-) GENECRAFT INC.
XX
PI Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;
XX
DR WPI; 2003-801317/75.
XX
PT New binding domain-immunoglobulin fusion protein, useful for treating a
PT subject having or suspected of having a malignant condition or a B-cell
PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.
XX
PS Disclosure; SEQ ID NO 64; 157pp; English.
XX
CC Unidentified
XX
SQ Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 2393;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
||||||||||||||||||
Db 78 GAGCAGGGCCATAATTAT 61

RESULT 10
ACA56611/c
ID ACA56611 standard; cDNA; 2393 BP.
XX
AC ACA56611;
XX
DT 06-JUN-2003 (first entry)
XX
DE Human signalling pathway polynucleotide probe SEQ ID NO 1209.
XX
KW Human; probe; ss; array element; Parkinson's disease;
KW signalling pathway population; cancer; adenocarcinoma; leukaemia;
KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
XX
OS Homo sapiens.
XX
PN US6500938-B1.
XX
PD 31-DEC-2002.
XX
PF 30-JAN-1998; 98US-00016434.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2003-352189/33.
XX
PT Combination of polynucleotide probes, useful as array elements in a
PT microarray for monitoring the expression of a number of target
PT polynucleotides.
XX
PS Claim 1; SEQ ID NO 1209; 65pp; English.
XX
CC The invention relates to a combination which, comprises a number of
CC polynucleotide probes comprising a sequence selected from one of the 1490
CC sequences mentioned in the specification. The combination is useful as an
CC array element in a microarray for monitoring the expression of a number
CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence represents a polynucleotide
CC probe of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 2393;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
||||||||||||||||||
Db 78 GAGCAGGGCCATAATTAT 61

RESULT 11
ADI56407/c
ID ADI56407 standard; DNA; 2393 BP.
XX
AC ADI56407;
XX
DT 22-APR-2004 (first entry)
XX
DE Human polynucleotide probe #1209.
XX
KW Human; probe; ss; receptor-like polypeptide; transducing polypeptide;
KW effector-like polypeptide; cancer; immunopathology; neuropathology;
KW drug development; toxicology; carcinogenicity;
KW signalling pathway polypeptide; adrenal gland; bladder; bone;
KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;
KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;
KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.
XX

OS Homo sapiens.
XX
PN US2004010136-A1.
XX
PD 15-JAN-2004.
XX
PF 26-NOV-2002; 2002US-00305720.
XX
PR 30-JAN-1998; 98US-00016434.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Au-Young J, Seilhamer JJ;
XX
DR WPI; 2004-090520/09.
XX
PT New composition comprising polynucleotide probes, useful as array
PT elements in a microarray for monitoring the expression of target
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic
PT fragments.
XX
PS Claim 6; SEQ ID NO 1209; 73pp; English.
XX
CC The invention relates to a composition of polynucleotide probes
CC comprising first polynucleotide probes comprising at least a portion of a
CC gene encoding a receptor-like polypeptide, second polynucleotide probes
CC comprising at least a portion of a gene encoding a transducing
CC polypeptide and third polynucleotide probes comprising at least a portion
CC of a gene encoding an effector-like polypeptide. The probes of the
CC composition are useful as array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray is useful in the
CC diagnosis and treatment of cancer, an immunopathology or a
CC neuropathology. It can also be used for drug discovery and development,
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.
CC Microarrays can also be used for monitoring the progression of diseases
CC that may be associated with the altered expression of signalling pathway
CC polypeptides. The composition can also be used to purify a subpopulation
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,
CC epilepsy, Alzheimer's disease or depression. This sequence represents a
CC human polynucleotide probe of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 2393;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAATTAT 18
||||||||||||||||||
Db 78 GAGCAGGGCCATAATTAT 61

RESULT 12
ADO29879/c
ID ADO29879 standard; cDNA; 2393 BP.
XX
AC ADO29879;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human GPCR FSHR polynucleotide, SEQ ID NO:981.
XX
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004040000-A2.
XX
PD 13-MAY-2004.
XX
PF 09-SEP-2003; 2003WO-US028226.
XX
PR 09-SEP-2002; 2002US-0409303P.
PR 09-APR-2003; 2003US-0461329P.
XX
PA (PRIM-) PRIMAL INC.
XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
DR WPI; 2004-390329/36.
DR P-PSDB; AD029321.
XX
PT Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX
PS Claim 151; SEQ ID NO 981; 542pp; English.
XX
CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the trasngenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2393 BP; 648 A; 596 C; 484 G; 665 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 12; Length 2393;

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  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         78 GAGCAGGGCCATAATTAT 61


RESULT 13
ADR26224
ID   ADR26224 standard; DNA; 507 BP.
XX
AC   ADR26224;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Breast cancer prognosis marker #2085.
XX
KW   ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO2004065545-A2.
XX
PD   05-AUG-2004.
XX
PF   15-JAN-2004; 2004WO-US001100.
XX
PR   15-JAN-2003; 2003US-00342887.
XX
PA   (ROSE-) ROSETTA INPHARMATICS LLC.
PA   (NECA-) NETHERLANDS CANCER INST.
XX
PI   Van't Veer LJ,  He Y;
XX
DR   WPI; 2004-593473/57.
XX
PT   Classifying a breast cancer patient according to prognosis comprises
PT   determining the similarity between the level of expression of each of
PT   five genes in a cell sample taken from patient, to control levels.
XX
PS   Disclosure; SEQ ID NO 2085; 226pp; English.
XX
CC   The invention relates to a method of classifying a breast cancer patient
CC   according to prognosis by determining the similarity between the level of
CC   expression of each of five genes for which markers are listed in the
CC   specification, in a cell sample taken from the breast cancer patient, to
CC   control levels of expression for each respective five genes to obtain a
CC   patient similarity value. The methods are useful for classifying a breast
CC   cancer patient according to prognosis. Kits and computer program products
CC   are useful for data analysis using the diagnostic, prognostic and
CC   statistical methods of the invention. This sequence corresponds to a
CC   marker used in the method of the invention.
XX
SQ   Sequence 507 BP; 151 A; 103 C; 90 G; 163 T; 0 U; 0 Other;

  Query Match             83.3%;  Score 15;  DB 13;  Length 507;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATT 16
              |||||||||||||||
Db        163 AGCAGGGCCATAATT 177


RESULT 14
ABT03390/c
ID   ABT03390 standard; DNA; 612 BP.
XX
AC   ABT03390;
XX
DT   28-NOV-2002  (first entry)
XX
DE   Ovary cell-specific DNA sequence 106.
XX
KW   Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
KW   ovary specific protein; ovarian cancer; breast cancer; ss; vaccine;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200238606-A2.
XX
PD   16-MAY-2002.
XX
PF   07-NOV-2001; 2001WO-US046459.
XX
PR   08-NOV-2000; 2000US-0246640P.
XX
PA   (DIAD-) DIADEXUS INC.
XX
PI   Sun Y,  Recipon H,  Salceda S,  Liu C;
XX
DR   WPI; 2002-519297/55.
XX
PT   Polypeptide and polynucleotides present in normal and neoplastic ovary
PT   cells, useful for identifying, monitoring, staging, diagnosing,
PT   preventing and treating ovarian cancer, and non-cancerous disease states
PT   in the ovary.
XX
PS   Claim 1; Page 192; 247pp; English.
XX
CC   The invention comprises amino acid and DNA sequences which are present in
CC   normal and neoplastic ovary cells. The DNA and protein sequences of the
CC   invention are useful for determining the presence of an ovary specific
CC   nucleic acid or an ovary specific protein in a sample. The DNA and
CC   protein sequences of the invention are useful for diagnosing and
CC   monitoring the presence and metastasis of ovarian cancer and breast
CC   cancer. Nucleotides ABT03285 - ABT03421 represents the ovary cell
CC   specific DNA sequences of the invention
XX
SQ   Sequence 612 BP; 202 A; 112 C; 108 G; 190 T; 0 U; 0 Other;

  Query Match             83.3%;  Score 15;  DB 6;  Length 612;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAATT 16
              |||||||||||||||
Db        303 AGCAGGGCCATAATT 289


RESULT 15
ABT03391/c
ID   ABT03391 standard; DNA; 628 BP.
XX
AC   ABT03391;
XX
DT   28-NOV-2002  (first entry)
XX
DE   Ovary cell-specific DNA sequence 107.
XX
KW   Ovary cell; neoplastic ovary cell; ovary specific nucleic acid;
KW   ovary specific protein; ovarian cancer; breast cancer; ss; vaccine;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200238606-A2.
XX
PD   16-MAY-2002.
XX
PF   07-NOV-2001; 2001WO-US046459.
XX
PR   08-NOV-2000; 2000US-0246640P.
XX
```

PA (DIAD-) DIADEXUS INC.
XX
PI Sun Y, Recipon H, Salceda S, Liu C;
XX
DR WPI; 2002-519297/55.
XX
PT Polypeptide and polynucleotides present in normal and neoplastic ovary
PT cells, useful for identifying, monitoring, staging, diagnosing,
PT preventing and treating ovarian cancer, and non-cancerous disease states
PT in the ovary.
XX
PS Claim 1; Page 192-193; 247pp; English.
XX
CC The invention comprises amino acid and DNA sequences which are present in
CC normal and neoplastic ovary cells. The DNA and protein sequences of the
CC invention are useful for determining the presence of an ovary specific
CC nucleic acid or an ovary specific protein in a sample. The DNA and
CC protein sequences of the invention are useful for diagnosing and
CC monitoring the presence and metastasis of ovarian cancer and breast
CC cancer. Nucleotides ABT03285 - ABT03421 represents the ovary cell
CC specific DNA sequences of the invention
XX
SQ Sequence 628 BP; 202 A; 115 C; 102 G; 209 T; 0 U; 0 Other;

Query Match 83.3%; Score 15; DB 6; Length 628;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCAGGGCCATAATT 16
||||||||||||||||
Db 319 AGCAGGGCCATAATT 305

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Job time : 227.5 secs

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OM nucleic - nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	18	100.0	2179	2	US-08-531-070A-1	Sequence 1, Appli
c	3	18	100.0	2179	3	US-08-482-855-1	Sequence 1, Appli
c	4	18	100.0	2179	3	US-08-474-986-1	Sequence 1, Appli
c	5	18	100.0	2393	3	US-09-016-434-1209	Sequence 1209, Ap
c	6	15	83.3	481	3	US-09-270-767-1666	Sequence 1666, Ap
c	7	15	83.3	481	3	US-09-270-767-16948	Sequence 16948, A
	8	15	83.3	52992	3	US-09-949-016-16105	Sequence 16105, A
c	9	14	77.8	900	3	US-09-489-039A-6996	Sequence 6996, Ap
c	10	14	77.8	1149	3	US-09-602-787A-379	Sequence 379, App
	11	14	77.8	1887	3	US-09-620-312D-42	Sequence 42, Appl
c	12	14	77.8	3678	3	US-09-112-580-13	Sequence 13, Appl
	13	14	77.8	3762	3	US-09-489-039A-4926	Sequence 4926, Ap
c	14	14	77.8	55264	3	US-09-949-016-15014	Sequence 15014, A
	15	14	77.8	70828	3	US-09-949-016-12122	Sequence 12122, A
c	16	14	77.8	94755	3	US-09-949-016-11839	Sequence 11839, A
c	17	14	77.8	101951	3	US-09-949-016-15648	Sequence 15648, A
c	18	14	77.8	137226	3	US-09-949-016-13763	Sequence 13763, A
	19	14	77.8	139936	3	US-09-949-016-11782	Sequence 11782, A
	20	14	77.8	139952	3	US-09-949-016-13280	Sequence 13280, A
c	21	14	77.8	147840	3	US-09-949-016-15236	Sequence 15236, A
c	22	13	72.2	25	3	US-09-396-196G-44948	Sequence 44948, A
c	23	13	72.2	339	3	US-09-489-039A-6054	Sequence 6054, Ap
	24	13	72.2	459	3	US-09-248-796A-1604	Sequence 1604, Ap
c	25	13	72.2	601	3	US-09-949-016-48726	Sequence 48726, A
	26	13	72.2	601	3	US-09-949-016-156620	Sequence 156620,
c	27	13	72.2	601	3	US-09-949-016-160355	Sequence 160355,
c	28	13	72.2	601	3	US-09-949-016-160356	Sequence 160356,
c	29	13	72.2	668	3	US-09-533-559-5223	Sequence 5223, Ap
c	30	13	72.2	886	2	US-08-469-427A-1	Sequence 1, Appli
c	31	13	72.2	886	2	US-08-609-443B-1	Sequence 1, Appli
c	32	13	72.2	886	2	US-08-569-063C-1	Sequence 1, Appli
c	33	13	72.2	886	3	US-08-851-896-1	Sequence 1, Appli
c	34	13	72.2	1443	3	US-09-489-039A-5874	Sequence 5874, Ap
c	35	13	72.2	2554	3	US-09-701-868-4	Sequence 4, Appli
	36	13	72.2	7883	3	US-09-949-016-13183	Sequence 13183, A
c	37	13	72.2	8773	3	US-09-949-016-14496	Sequence 14496, A
	38	13	72.2	9792	3	US-09-635-872A-14	Sequence 14, Appl
	39	13	72.2	9792	3	US-09-636-077A-14	Sequence 14, Appl
	40	13	72.2	9792	3	US-09-636-060C-14	Sequence 14, Appl
	41	13	72.2	9792	3	US-09-986-552-14	Sequence 14, Appl
	42	13	72.2	9792	3	US-09-636-596C-14	Sequence 14, Appl
	43	13	72.2	9792	3	US-10-023-894-21	Sequence 21, Appl
	44	13	72.2	9792	3	US-10-306-686-14	Sequence 14, Appl
	45	13	72.2	9792	3	US-09-895-072-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-487-886-1/c
; Sequence 1, Application US/08487886
; Patent No. 5744448
; GENERAL INFORMATION:
; APPLICANT: Kelton, Christie Ann
; APPLICANT: Schweickhardt, Rene Lynn
; APPLICANT: Cheng, Shirley Vui Yen
; APPLICANT: Nugent, No. 5744448een Patrice
; TITLE OF INVENTION: Human Follicle Stimulating
; TITLE OF INVENTION: Hormone Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephan P. Williams,
; ADDRESSEE: Ares-Serono, Inc.
; STREET: Exchange Place, 37th floor
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
; COMPUTER: IBM PS/2, model 55 SX
; OPERATING SYSTEM: MS-DOS version 4.0
; SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/670,085
; FILING DATE: 15-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Stephan P.
; REGISTRATION NUMBER: 28546
; REFERENCE/DOCKET NUMBER: US/252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-1300
; TELEFAX: (617) 723-8923
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2179
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:

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;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  Testis
;    IMMEDIATE SOURCE:
;      LIBRARY:  lgt11 cDNA library, ClonTech #HL1010b
;      CLONE:  pHFSHR11-11, pHFSHR15-6
;    FEATURE:
;      NAME/KEY:  protein coding region
;      LOCATION:  75 to 2159
US-08-487-886-1

  Query Match             100.0%;  Score 18;  DB 2;  Length 2179;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         86 GAGCAGGGCCATAATTAT 69


RESULT 2
US-08-531-070A-1/c
; Sequence 1, Application US/08531070A
; Patent No. 5851768
;  GENERAL INFORMATION:
;    APPLICANT:  de la Chapelle, Albert
;    APPLICANT:  Aittomaki, Kristiina
;    APPLICANT:  Huhtaniemi, Ilpo
;    TITLE OF INVENTION:  Method For Diagnosis Of Ovarian Dysgenesis
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/531,070A
;      FILING DATE:  20-SEP-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gass, David A.
;      REGISTRATION NUMBER:  38,153
;      REFERENCE/DOCKET NUMBER:  28113/32879
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2179 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-531-070A-1

  Query Match             100.0%;  Score 18;  DB 2;  Length 2179;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         86 GAGCAGGGCCATAATTAT 69


RESULT 3
US-08-482-855-1/c
; Sequence 1, Application US/08482855
; Patent No. 6121016
;  GENERAL INFORMATION:
;    APPLICANT:  Kelton, Christie Ann
;    APPLICANT:  Schweickhardt, Rene Lynn
;    APPLICANT:  Cheng, Shirley Vui Yen
;    APPLICANT:  Nugent, No. 6121016een Patrice
;    TITLE OF INVENTION:  Human Follicle Stimulating
;    TITLE OF INVENTION:  Hormone Receptor
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Stephan P. Williams,
;      ADDRESSEE:  Ares-Serono, Inc.
;      STREET:  Exchange Place, 37th floor
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" diskette, 1.44 MB, high density
;      COMPUTER:  IBM PS/2, model 55 SX
;      OPERATING SYSTEM:  MS-DOS version 4.0
;      SOFTWARE:  VAX/VMS Mass11 via Kermit to IBM MS-DOS
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,855
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/670,085
;      FILING DATE:  15-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Williams, Stephan P.
;      REGISTRATION NUMBER:  28546
;      REFERENCE/DOCKET NUMBER:  US/252
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 723-1300
;      TELEFAX:  (617) 723-8923
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2179
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  Testis
;    IMMEDIATE SOURCE:
;      LIBRARY:  lgt11 cDNA library, ClonTech #HL1010b
;      CLONE:  pHFSHR11-11, pHFSHR15-6
;    FEATURE:
;      NAME/KEY:  protein coding region
;      LOCATION:  75 to 2159
US-08-482-855-1

  Query Match             100.0%;  Score 18;  DB 3;  Length 2179;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         86 GAGCAGGGCCATAATTAT 69


RESULT 4
US-08-474-986-1/c
; Sequence 1, Application US/08474986
; Patent No. 6372711
;  GENERAL INFORMATION:
;       APPLICANT: Kelton, Christie Ann
;                  Schweickhardt, Rene Lynn
;                  Cheng, Shirley Vui Yen
;                  Nugent, No. 6372711een Patrice
```

```
;       TITLE OF INVENTION: Human Follicle Stimulating
;                           Hormone Receptor
;       NUMBER OF SEQUENCES: 2
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Stephan P. Williams,
;                       Ares-Serono, Inc.
;            STREET: Exchange Place, 37th floor
;            CITY: Boston
;            STATE: MA
;            COUNTRY: USA
;            ZIP: 02109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
;            COMPUTER: IBM PS/2, model 55 SX
;            OPERATING SYSTEM: MS-DOS version 4.0
;            SOFTWARE: VAX/VMS Mass11 via Kermit to IBM MS-DOS
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/474,986
;            FILING DATE: 07-Jun-1995
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 07/670,085
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Williams, Stephan P.
;            REGISTRATION NUMBER: 28546
;            REFERENCE/DOCKET NUMBER: US/252
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617) 723-1300
;            TELEFAX: (617) 723-8923
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2179
;            TYPE: Nucleic acid
;            STRANDEDNESS: Double
;            TOPOLOGY: Linear
;       MOLECULE TYPE: cDNA to mRNA
;       ORIGINAL SOURCE:
;            ORGANISM: Homo sapiens
;            TISSUE TYPE: Testis
;       IMMEDIATE SOURCE:
;            LIBRARY: lgt11 cDNA library, ClonTech #HL1010b
;            CLONE: pHFSHR11-11, pHFSHR15-6
;       FEATURE:
;            NAME/KEY:  protein coding region
;            LOCATION:  75 to 2159
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-474-986-1

  Query Match             100.0%;  Score 18;  DB 3;  Length 2179;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         86 GAGCAGGGCCATAATTAT 69


RESULT 5
US-09-016-434-1209/c
; Sequence 1209, Application US/09016434
; Patent No. 6500938
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1209:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2393 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g182770
US-09-016-434-1209

  Query Match             100.0%;  Score 18;  DB 3;  Length 2393;
  Best Local Similarity   100.0%;  Pred. No. 0.21;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAATTAT 18
              ||||||||||||||||||
Db         78 GAGCAGGGCCATAATTAT 61


RESULT 6
US-09-270-767-1666/c
; Sequence 1666, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1666
;   LENGTH: 481
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-1666

  Query Match             83.3%;  Score 15;  DB 3;  Length 481;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAAT 15
              |||||||||||||||
Db        199 GAGCAGGGCCATAAT 185


RESULT 7
US-09-270-767-16948/c
; Sequence 16948, Application US/09270767
; Patent No. 6703491
```

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; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16948
;   LENGTH: 481
;   TYPE: DNA
;   ORGANISM: Drosophila melanogaster
US-09-270-767-16948

  Query Match             83.3%;  Score 15;  DB 3;  Length 481;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAAT 15
              |||||||||||||||
Db        199 GAGCAGGGCCATAAT 185


RESULT 8
US-09-949-016-16105
; Sequence 16105, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16105
;   LENGTH: 52992
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-16105

  Query Match             83.3%;  Score 15;  DB 3;  Length 52992;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CAGGGCCATAATTAT 18
              |||||||||||||||
Db       1227 CAGGGCCATAATTAT 1241


RESULT 9
US-09-489-039A-6996/c
; Sequence 6996, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;  APPLICANT:  Gary Breton et. al
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;  TITLE OF INVENTION:  PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  2709.2004001
;  CURRENT APPLICATION NUMBER: US/09/489,039A
;  CURRENT FILING DATE:  2000-01-27
;  PRIOR APPLICATION NUMBER:  US 60/117,747
;  PRIOR FILING DATE:  1999-01-29
;  NUMBER OF SEQ ID NOS:  14342
; SEQ ID NO 6996
;   LENGTH: 900
;   TYPE: DNA
;   ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6996

  Query Match             77.8%;  Score 14;  DB 3;  Length 900;
  Best Local Similarity   100.0%;  Pred. No. 45;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 AGCAGGGCCATAAT 15
              ||||||||||||||
Db        137 AGCAGGGCCATAAT 124


RESULT 10
US-09-602-787A-379/c
; Sequence 379, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT:  Kr"ger, Burkhard
;  APPLICANT:  Sch"der, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION:  TRANSPORT
;  FILE REFERENCE: BGI-125CP
;  CURRENT APPLICATION NUMBER: US/09/602,787A
;  CURRENT FILING DATE:  2000-06-23
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932182.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932190.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932191.4
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932209.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932212.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932227.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932228.7
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932229.5
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932230.9
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932927.3
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933005.0
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19933006.9
;  PRIOR FILING DATE: 1999-07-14
;  PRIOR APPLICATION NUMBER: DE 19940764.9
;  PRIOR FILING DATE: 1999-08-27
```

; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 379
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1126)
; OTHER INFORMATION: RXN00523
US-09-602-787A-379

Query Match 77.8%; Score 14; DB 3; Length 1149;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCAGGGCCATAA 14
||||||||||||||
Db 242 GAGCAGGGCCATAA 229

RESULT 11
US-09-620-312D-42
; Sequence 42, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 42
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(1563)
US-09-620-312D-42

Query Match 77.8%; Score 14; DB 3; Length 1887;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGCAGGGCCATAAT 15
||||||||||||||
Db 883 AGCAGGGCCATAAT 896

RESULT 12
US-09-112-580-13/c
; Sequence 13, Application US/09112580
; Patent No. 6610539
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping
; APPLICANT: DUGOURD, Dominique
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF
; TITLE OF INVENTION: MICROORGANISMS
; FILE REFERENCE: 032396-016
; CURRENT APPLICATION NUMBER: US/09/112,580
; CURRENT FILING DATE: 1998-07-09
; EARLIER APPLICATION NUMBER: US 60/052,160
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 265
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 3678
; TYPE: DNA
; ORGANISM: Equine herpesvirus 4
US-09-112-580-13

Query Match 77.8%; Score 14; DB 3; Length 3678;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AGGGCCATAATTAT 18
||||||||||||||
Db 2492 AGGGCCATAATTAT 2479

RESULT 13
US-09-489-039A-4926
; Sequence 4926, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4926
; LENGTH: 3762
; TYPE: DNA

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;   ORGANISM: Klebsiella pneumoniae
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1044),(1659)
;   OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-489-039A-4926

  Query Match             77.8%;  Score 14;  DB 3;  Length 3762;
  Best Local Similarity   100.0%;  Pred. No. 45;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCAGGGCCATAA 14
              ||||||||||||||
Db       3709 GAGCAGGGCCATAA 3722


RESULT 14
US-09-949-016-15014/c
; Sequence 15014, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15014
;   LENGTH: 55264
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-15014

  Query Match             77.8%;  Score 14;  DB 3;  Length 55264;
  Best Local Similarity   100.0%;  Pred. No. 45;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      41078 CAGGGCCATAATTA 41065


RESULT 15
US-09-949-016-12122
; Sequence 12122, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12122
;   LENGTH: 70828
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(70828)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12122

  Query Match             77.8%;  Score 14;  DB 3;  Length 70828;
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Db      35400 CAGGGCCATAATTA 35413


Search completed: November 29, 2005, 18:24:59
Job time : 73 secs
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